

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 21:50:17 ; Search time 2304 Seconds
(without alignments)
9199.107 Million cell updates/sec

Title: US-09-773-476-294
Perfect score: 489
Sequence: 1 gactgagctagatcttcag.....tnatgagccacacaagactt 489

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_pl.*
8: gb_pr.*
9: gb_ro.*
10: gb_sy.*
11: gb_sts.*
12: gb_un.*
13: gb_vl.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pin.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	471.4	96.4	979	10	BC057097	BC057097 Mus muscu
2	470.4	96.2	896	10	BC049637	BC049637 Mus muscu
3	353	72.2	905	6	BD076403	BD076403 Homo sapi
4	353	72.2	922	9	BC002846	BC002846 Homo sapi
5	353	72.2	932	6	AX055686	AX055686 Sequence
6	353	72.2	932	6	AX076904	AX076904 Sequence
7	353	72.2	932	6	AX077021	AX077021 Sequence
8	353	72.2	932	6	AX574480	AX574480 Sequence
9	353	72.2	932	9	AY358968	AY358968 Homo sapi
10	353	72.2	940	9	BC011006	BC011006 Homo sapi
11	353	72.2	970	9	BC035850	BC035850 Homo sapi
12	353	72.2	1056	9	BC021237	BC021237 Homo sapi
13	353	72.2	1265	6	BD276564	BD276564 EXTRACELL
14	353	72.2	1265	6	AX048198	AX048198 Sequence
15	351.4	71.9	915	9	AF275744	AF275744 Homo sapi
16	344	70.3	687	6	BD076393	BD076393 Homo sapi
17	340.4	69.6	1074	9	AF144055	AF144055 Homo sapi
18	287.6	58.8	512	6	AX395873	AX395873 Sequence
19	256.2	52.4	549	6	AX395797	AX395797 Sequence
20	254.6	52.1	529	6	AX778895	AX778895 Sequence
21	182.6	37.3	524	6	AR413766	AR413766 Sequence
22	182.6	37.3	524	6	BD109319	BD109319 EST and e
23	173.2	35.4	486	6	AX552302	AX552302 Sequence
24	165	33.7	498	6	AR415192	AR415192 Sequence
25	165	33.7	498	6	BD110745	BD110745 EST and e
26	146.8	30.0	459	6	AX884298	AX884298 Sequence
27	146.8	30.0	459	6	BD023908	BD023908 Sequence
28	139.8	28.6	462	6	AX874501	AX874501 Primer fo
29	139.8	28.6	462	6	BD154563	BD154563 Mus muscu
30	123.8	25.3	209211	2	AC084883	AC084883 Mus muscu
31	123.8	25.3	216195	10	AC109608	AC109608 Mus muscu
32	113.6	23.2	180005	2	AC112904	AC112904 Rattus no
33	113.6	23.2	264108	2	AC126142	AC126142 Rattus no
34	113.6	23.2	274060	2	AC095184	AC095184 Rattus no
35	104	21.3	1671	10	HAWCAD	M31621 Syrian hams
36	92.8	19.0	64476	2	AC124292	AC124292 Homo sapi
37	92.8	19.0	159707	9	AC013403	AC013403 Homo sapi
38	90.2	18.4	123280	2	AC025662	AC025662 Homo sapi
39	86.4	17.7	2056	9	AF015947	AF015947 Homo sapi
40	66.8	13.7	180005	2	AC112904	AC112904 Rattus no
41	45.4	9.3	452	6	AR424977	AR424977 Sequence
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43	41.6	8.5	167149	5	EX276101	EX276101 Zebrafish
44	41.2	8.4	310787	2	AC125297	AC125297 Rattus no
45	39	8.0	50	6	AX055746	AX055746 Sequence

ALIGNMENTS

RESULT 1
BC057097 979 bp mRNA linear ROD 08-OCT-2003
LOCUS Mus musculus cDNA clone MGC:61368 IMAGE:5714599, complete cds.
DEFINITION BC057097
ACCESSION BC057097.1 GI:34785321
VERSION MGC.
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 979)
REFERENCE
AUTHORS
Straussberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, A.A., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 979)

Strausberg, R.

Direct Submission

Submitted (28-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-i@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library Preparation: M. Bento Soares, University of Iowa

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.

Web site: <http://genome.uiowa.edu>

Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu

Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A., Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K., Scheetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J., Casavant, T., Soares, M.B.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: Location/Qualifiers

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/clone_lib="NIH_BMAP_PB0"

/lab_host="DH10B"

/notes="Vector: pYX-ASC"

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CDS

Query March

Best Local Similarity 99.2%; Pred. No. 2.1e-146; Length 979;

Matches 483; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCTG-AGGATCCTGTCCTCAAACTTTTACAGGCTT 62

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Db 206 TGGGCTAGATCTTCAGAACTGTTCCCTGGAAGGATCCTGGTCCAAACTTTTACAGGCTT 265

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Db 266 ATATCGCTATTATCATAGACCTTCAGGCAAACTCCTCTCAAGGATGATTGGCCCAACACCT 325

QY 123 TCCGTTGGTGTACTCAGCTGCGAGACTCTGTATACCAAGAGATGTTCCCTGTCTCTGGAG 182

Db 326 TCCGTTGGTGTACTCAGCTGCGAGACTCTGTATACCAAGAGATGTTCCCTGTCTCTGGAG 385

QY 183 GTAGTAATGCTCGGACAACTGTTACTCTTTCAGAGCAACAGCAGATTTGCCAAGGGCAAA 242

Db 386 GTAGTAATGCTCGGACAACTGTTACTCTTTCAGAGCAACAGCAGATTTGCCAAGGGCAAA 445

QY 243 GGGACCTTTGCAATAGCACTGGAAGCCGAGAAATGTGTCTGAGAACGGATCTTGTGCAT 302

Db 446 GGGACCTTTGCAATAGCACTGGAAGCCGAGAAATGTGTCTGAGAACGGATCTTGTGCAT 505

QY 303 CTGACGGTCTCTGTTCTTTTGCAGTCCGTTTGTCTGATGTTTCCATGGATACAGTGTA 362

Db 506 CTGACGGTCTCTGTTCTTTTGCAGTCCGTTTGTCTGATGTTTCCATGGATACAGTGTA 565

QY 363 TGAGCAGGGGCTCATTTTCACTGCTTATGTTCTTTGGGATTTCTGGGATCCACACGGTAG 422

Db 566 TGAGCAGGGGCTCATTTTCACTGCTTATGTTCTTTGGGATTTCTGGGATCCACACGGTAG 625

QY 423 CCATCTNCAATCTACTTTTGGGACCCAGCCGAGAAAGCCGAGAAAGCCGAGCTTATGAGCCAC 482

Db 626 CCATCTNCAATCTACTTTTGGGACCCAGCCGAGAAAGCCGAGCTTATGAGCCAC 685

QY 483 AAGACTT 489

Db 686 AAGACTT 692

RESULT 2

BC049637

LOCUS

DEFINITION

Mus musculus mRNA similar to apoptosis related protein APR-3 (cdna clone MGC:58396 IMAGE:6585654), complete cds.

ACCESSION

BC049637.1 GI:29437024

VERSION

MGC.

KEYWORDS

Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 896)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., McKernan, K.J., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 896)

Strausberg, R.

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE
JOURNAL

REMARK
COMMENT

Direct Submission
Submitted (31-MAR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein / Ted Usdin
Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Teai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 45 Row: d Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
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AS"

ORIGIN
Query Match 96.2%; Score 470.4; DB 10; Length 896;
Best Local Similarity 99.2%; Pred. No. 4.4e-146;
Matches 482; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 5 GAGGCTAGATCTTCAGAACTGTTCCTG-AGGATCTGTGTCACAACTTTTACAGGCTTA 63
Db 118 GAGGCTAGATCTTCAGAACTGTTCCTGAGGATCTGTGTCACAACTTTTACAGGCTTA 177
QY 64 TACTGCTATTATCATAGACTTCAGGCAAACTCTCAAGGATGATTTGGCCAAACACCTT 123
Db 178 TACTGCTATTATCATAGACTTCAGGCAAACTCTCAAGGATGATTTGGCCAAACACCTT 237
QY 124 CCCTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGAGTGTTCCTGCTCGGAGG 183
Db 238 CCCTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGAGTGTTCCTGCTCGGAGG 297
QY 184 TAGTAATGCTGGGCAAACTTTACTTCTTTCAAGGACAAAGCAGATTGGCAAGGGCAAG 243
Db 298 TAGTAATGCTGGGCAAACTTTACTTCTTTCAAGGACAAAGCAGATTGGCAAGGGCAAG 357
QY 244 GGAACCTTTGCAATAGACTGGAAGCCGAGAAATGTGTCTTGAGAACGATTTGTGTCATC 303

Db 358 GGACCTTTGCAATAGCACTGGAAGCCAGAAATGTGTCTCTGAGAACGATCTTTGTGCATC 417
QY 304 TGACGGTCCCTGGTCTTTTTCAGTGCCTTCTGCTGTGATGGTTTCCATGATACAAAGTGTAT 363
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QY 484 AGACTT 489
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RESULT 3
BD076403
LOCUS
DEFINITION Human protein having transmembrane domain and DNA encoding the same.
BD076403
ACCESSION BD076403.1 GI:22622006
VERSION BD076403.1 JP 2001519154-A/17.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Kato, S., Kimura, T., Sekine, S. and Kobayashi, M.
AUTHORS Human protein having transmembrane domain and DNA encoding the same
TITLE Patent: JP 2001519154-A 17 23-OCT-2001;
JOURNAL SAGAMI CHEMICAL RESEARCH CENTER, PROTEGENE INC
COMMENT OS Homo sapiens (human)
PN JP 2001519154-A/17
PF 23-OCT-2001
PP 05-OCT-1998 JP 2000515001
PI SEISHI KATO, TOMOKO KIMURA, SHINGO SEKINE, MIDORI KOBAYASHI PC
C12N15/09, C07K14/47, C12N5/10, C12N15/00, C12N5/00 CC Human protein
having transmembrane domain
and DNA encoding the
same
CC Key Location/Qualifiers
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FT /organism="Homo sapiens (human)".
FT Location/Qualifiers
source 1..905
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/mol_type="genomic DNA"
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ORIGIN
Query Match 72.2%; Score 353; DB 6; Length 905;
Best Local Similarity 84.0%; Pred. No. 1.1e-106;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
QY 4 TGAGCTAGATCTTCAGAACTGTTCCTT-GAGGATCTGTGTCACAACTTTTACAGGCTT 62
Db 226 TGGGCTGGATCTCCAGAACTGTTCCTCTGGAGGACCCCTGGTCCAAACTTTTCATCAGGCAC 285
QY 63 ATACTGCTATTATCATAGACTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACACCT 122
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Db 346 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGAGTGTTCCTGTCTCGAG 405
QY 183 GTAGTAATGCTGGGCAAACTTACTTCTTTCAAGGACCAAGCAGATTTGCCAAGGGCAA 242

Db 406 GAATTAATGCTCGGATACATACCTCTTATATAGAACCAAAATCTGTCAAGGGCAAA 465
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QY 363 TGAGGACGGCTCAATTTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 422
Db 586 TGCCGCCAGGGCTCGTTCTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 645
QY 423 CCATCTTCATCTACTTTTGGGGAACCCAGCGCCGGAAGCCAAAGCTTTNATGAGCCAC 482
Db 646 CCGTCTCCATCTCTTTTGGGCGACCCAGCGCCGGAAGCCAAAGCTTTNATGAGCTACAT 705
QY 483 AAGACTT 489
Db 706 AGGTCTT 712

RESULT 4
LOCUS BC002846
DEFINITION Homo sapiens apoptosis related protein APR-3, transcript variant 2,
mRNA (cDNA clone MGC:3348 IMAGE:3635746), complete cds.
ACCESSION BC002846
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 922)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Spapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Sheezy, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S., Locuelli, N.A., Peters, G.J.,
Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vallalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E.,
Schnierch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)
2238257
12477932
2 (bases 1 to 922)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),
Gaithersburg, Maryland.
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mgc@nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgenev, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 12 Row: n Column: 8
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 18105011.

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ORIGIN
Query Match 72.2%; Score 353; DB 9; Length 922;
Best Local Similarity 84.0%; Pred. No. 1.le-106;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
QY 4 TCAGGCTAGATCTTCAGAACTGTTCCTT-GAGGATCTGTTCCTTTCAGAGCTT 62
Db 224 TGGGCTGGATCTCCAGAACTGTTCCTGAGGAGACCTGTGTCCTTTCATCAGGCAC 283
QY 63 ATATGCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCAAACCT 122
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VERSION AX077021.1 GI:13121656
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
AUTHORS Ashkenazi,A.J., Baker,K.P., Pong,S., Goddard,A., Godowski,P.J.,
Gurney,A.L., Hillan,K.J., Mark,M.R., Marsters,S.A., Pitti,R.M.,
Tumas,D., Watanabe,C.K. and Wood,W.I.
TITLE Compositions and methods for the treatment of immune related
diseases
JOURNAL Patent: WO 0105972-A 9 25-JAN-2001;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 72.2%; Score 353; DB 6; Length 932;
Best Local Similarity 84.0%; Pred. No. 1.1e-106;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TGAGGCTAGATCTTCAGAACTGTTCCTT-GAGGATCCTGTCCTCAAACTTTTACAGGCTT 62
Db 229 TGGGCTGGATCTCCAGAACTGTTCCTCTGGAGGACCTTGGTCCAACTTTTCATCAGGCAC 288
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QY 303 CTGACGGTCTGCTTTTTCAGTGCGTTTGTCTGATGTTTCCATGGATACAAAGTGA 362
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RESULT 9
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DEFINITION Homo sapiens
ACCESSION AY358968
VERSION AY358968.1 GI:37183053
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 932)
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heidens,S., Huang,A., Kim,H.S., Klimowski,L., Jit,Y., Johnson,S.,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Baker,K.P., Eaton,D.L., Filvaroff,E., Goddard,A., Grimaldi,J.C.,
Gurney,A.L., Smith,V., Stephan,J.P., Watanabe,C.K., Wood,W.I.,
Zhang,Z. and Pong,S.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0224888-A 7 28-MAR-2002;
Genentech, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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ORIGIN
Query Match 72.2%; Score 353; DB 6; Length 932;
Best Local Similarity 84.0%; Pred. No. 1.1e-106;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TGAGGCTAGATCTTCAGAACTGTTCCTT-GAGGATCCTGTCCTCAAACTTTTACAGGCTT 62
Db 229 TGGGCTGGATCTCCAGAACTGTTCCTCTGGAGGACCTTGGTCCAACTTTTCATCAGGCAC 288
QY 63 ATACTGCTATTATCATAGACTTCAGGCAAACTCTCTCAAGGATGATTGGCCCAACCT 122
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Db 589 TGGCCAGGGCTCGTCTCACTGCTTATGTTTCTTGGGATTCCTGGAGCCACCTCTAT 648
QY 423 CCATCTNCATTTCTACTTTGGGACCCAGCGCCGGAAGCCAGGCTTATGAGCCACAC 482
Db 649 CCGTCTCCATTTCTGTTTGGGCGACCCAGCGCCGGAAGCCAGGCTTATGAGCCACAT 708
QY 483 AAGACTT 489
Db 709 AGGTCTT 715

RESULT 8
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LOCUS Homo sapiens
DEFINITION Sequence 7 from Patent WO0224888.
ACCESSION AX574480
VERSION AX574480.1 GI:27551793
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vanden, R., Watanabe, C., Wiedand, D., Woods, K., Xie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I., and Godowski, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment

JOURNAL
PUBMED
12975309

REFERENCE
2 (bases 1 to 932)

AUTHORS
Clark, H.F.

TITLE
Direct Submission

JOURNAL
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,

Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES
Location/Qualifiers

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WATQRKAKTS"

ORIGIN

Query Match

Best Local Similarity 72.2%; Score 353; DB 9; Length 932;

Matches 409; Conservative 84.0%; Pred. No. 1,le-106;

Mismatches 0; Gaps 1; Indels 1; Gaps 1;

4 TGAGGCTAGATCTTCAGACTGTTCCT-GAGATCTGTCGTCACACTTTTACAGGCTT 62

229 TGGGGCTGGATCTCCAGACTGTTCCTGAGGACCTGTCGTCACACTTTTACAGGCTT 288

63 ATACTCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCACACCT 122

289 ATACCACTGTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCACACCT 348

123 TCGTGGGTTTACTCAGCTCAGACTCTGATACCAAGATGTCCTCTCTGGAG 182

349 TCGTGGGTTTACTCAGCTCAGACTCTGATACCAAGATGTCCTCTCTGGAG 408

183 GTAGTAATCGCTGGGCAATGTTACTTCTTCAAGGACAGAGATTTGCCAGGCAAA 242

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469 AGAACCTTTGCAATAGCACTTGGGCAATGTTCTCTGAGATGATCTTGTGCAAT 528

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589 TGGCCAGGCTGTTTCTACTGCTTATGTTCTTGGGATCTTGGGATCCACACCTAT 648

423 CCAATCTNCAATCTTACTTGGGCAATCCAGCGCGGAAAGCCAGGCTTATGAGCCAC 482

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Db 709 AGGTCTT 715

RESULT 10

LOCUS

DEFINITION
BC011006

ACCESSION
BC011006

VERSION
MGC

KEYWORDS
Homo sapiens (human)

SOURCE
Homo sapiens

ORGANISM
Homo sapiens

REFERENCE
1 (bases 1 to 940)

AUTHORS
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Mak, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., R.A.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,

Schneerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE

JOURNAL

MEDLINE

PUBMED

2 (bases 1 to 940)

Strausberg, R.

Direct Submission

Submitted (25-JUL-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

REMARK

COMMENT

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>

contact: amadan@systemsbiology.org

Manup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha

Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 19 Row: F Column: 23

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 18105011.

Location/Qualifiers

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WATQRRKAKTS"

ORIGIN
Query Match 72.2%; Score 353; DB 9; Length 940;
Best Local Similarity 84.0%; Pred. No. 1.le-106;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

Qy 4 TGAGGCTAGATCTTCAGAACTGTTCCTT-CAGGATCTGTGTCGAACTTTTACAGGCTT 62
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RESULT 11
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BC035850
VERSION
BC035850.1 GI:23272697
KEYWORDS
MGC.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 970)
AUTHORS
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
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Klausner,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2. (bases 1 to 970)
Direct Submission
Strausberg,R.
Submitted (31-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Ahter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Graniter,S., Guan,J., Gupta,J., Hagniggi,F.,
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Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
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Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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mRNA (CDNA clone MGC:15159 IMAGE:4303513), complete cds.	
ACCESSION	
BC021237	
VERSION	
BC021237.2 GI:33991290	
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
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REFERENCE	
AUTHORS	
Klausner, R.D., Collins, F.S., Wagner, L., Shenn, C.M., Schuler, G.D.,	
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,	
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,	
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Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,	
Bouffard, G., Blakesley, R.W., Touchman, J.W., Green, E.D.,	
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,	
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Snaius, D.E.,	
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.	
Generation and initial analysis of more than 15,000 full-length	
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
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Strausberg, R.	
Direct Submission	
Submitted (14-JAN-2002) National Institutes of Health, Mammalian	
Gene Collection (MGC), Cancer Genomics Office, National Cancer	
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	
USA	
NIH-MGC Project URL: http://mgc.nci.nih.gov	
On Aug 20, 2003 this sequence version replaced gi:18204610.	
Contact: MGC help desk	
Email: gcgaps-r@mail.nih.gov	
Tissue Procurement: ATCC	
cDNA Library Preparation: Rubin Laboratory	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)	
DNA Sequencing by: National Institutes of Health Intramural	
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Gaithersburg, Maryland;	
Web site: http://www.nisc.nih.gov/	
Contact: nisc_mgc@nhgri.nih.gov	
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,	
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Clone distribution: MGC clone distribution information can be found	
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WATQRKAKTS"	
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Query Match	72.2%; Score 353; DB 9; Length 1056;
Best Local Similarity	84.0%; Pred. No. 1.1e-106;
Matches 409; Conservative	0; Mismatches 77; Indels 1; Gaps 1;

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DEFINITION EXTRACELLULAR SIGNALING MOLECULES.
ACCESSION BD276564
VERSION BD276564.1 GI:33086332
KEYWORDS JP 2002543840-A/12.
SOURCE Homo sapiens (human)
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REFERENCE 1 (bases 1 to 1265)
AUTHORS Patterson,C., Lu,D.A.M., Azimzai,Y., Mariah, Baughn,R., Lal,P.,
Bandman,O., Burford,N., Yue,H. and Tang,T.Y.
TITLE EXTRACELLULAR SIGNALING MOLECULES
JOURNAL Patent: JP 2002543840-A 12 24-DEC-2002;
INCYTE GENOMICS INC,TOM Y TANG,HENRY YUE,PREETI LAL,NEIL BURFORD,
OLGA BANDMAN,MARIAH R BAUGHN,YALDA AZIMZAI,DYUNG AINA M LU, CHANDRA
PATTERSON
COMMENT OS Homo sapiens
PN JP 2002543840-A/12
PD 24-DEC-2002
PF 19-MAY-2000 JP 2000618455
PR 04-OCT-1999 US 60/157508,30-JUL-1999 US 60/146700, PR
15-JUL-1999 US 60/144270,19-MAY-1999 US 60/134949 PI
chandra patterson,dyung aina m lu,yalda azimzai,mariah pi
baughn,preeti lal,
pi olga bandman,neil burford,henry yue,tom y tang CC This
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DEFINITION Sequence 38 from Patent WO0070049.
ACCESSION AX048198
VERSION AX048198.1 GI:11876988
KEYWORDS Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Tang,Y.T., Yue,H., Lal,P., Burford,N., Bandman,O., Baughn,M.R.,
Azimzai,Y., Lu,D.A. and Patterson,C.
TITLE Extracellular signaling molecules
JOURNAL Patent: WO 0070049-A 38 23-NOV-2000;
INCYTE GENOMICS, INC. (US)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Yang Y.C., Chen,S.Y. and Chang,M.S.
TITLE
Cloning and characterization of p18
JOURNAL
Unpublished
2 (bases 1 to 915)
Yang,Y.C., Chen,S.Y. and Chang,M.S.
AUTHORS
Direct Submission
TITLE
Submitted (06-JUN-2000) Dept. of Medical Research, Mackey Memorial
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GenCore version 5.1.6
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ALIGNMENTS

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XX DT 14-JUL-1999 (first entry)

XX DE Human transmembrane protein coding sequence, HP10435.

XX KW Transmembrane protein; human; cell membrane; proliferation; diagnosis;
cell differentiation; carcinostatic agent; probe; gene therapy;
XX KW signal transduction; apoptosis; inhibitor;
XX KW phosphatidyethanolamine N-methyltransferase; ss.

XX OS Homo sapiens.

XX PN WO9918203-A2.

XX PD 15-APR-1999.

XX PF 05-OCT-1998; 98WO-JF004475.

XX PR 08-OCT-1997; 97JP-00276271.

XX PA (SAGA) SAGAMI CHEM RES CENT.

XX PI (PROT-) PROTEGENE INC.

XX DR Kato S, Yamaguchi T, Sekine S, Kobayashi M;

XX WPI; 1999-277268/23.

XX P-PSDB; AAY13944.

XX PT Human transmembrane proteins and nucleotide sequences.

XX Claim 4; Page 125-126; 139pp; English.

XX CC This sequence encodes a human transmembrane protein of the invention. All
of the proteins exist in the cell membrane, so are considered to be
proteins controlling the proliferation and differentiation of the cells.
XX CC They may be useful as carcinostatic agents or as antigens for preparing
antibodies against the proteins. The cDNAs can be used as probes for gene
diagnosis and gene sources for gene therapy, as well as for large-scale
expression of the proteins. The HP01498 (see AAY13939) protein may be
associated with signal transduction associated with apoptosis, and
therefore useful in inhibition of apoptosis. The HP01962 (see AAY13943)

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QY 423 CCATCTNCATTTACTTTGGGAACCCAGCGCGGAAAGCCAAAGCTTATGAGCCAC 482
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QY 483 AAGACTT 489
Db 702 AGGTCTT 708

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ID AAS08543 standard; cDNA; 923 BP.
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DT 24-OCT-2001 (first entry)
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KW diagnostic; therapeutic; immune disorder; multiple sclerosis;
KW systemic lupus erythematosus; human immuno-deficiency virus; HIV;
KW hyperproliferative disorder; Gaucher's disease; cardiovascular disease;
KW Scimitar syndrome; Chaga's cardiomyopathy; coronary arteriosclerosis;
KW angiogenic disorder; corneal graft; neovascularisation; wound healing;
KW diabetic retinopathy; neurological disorder; Huntington's chorea;
KW Alzheimer's disease; Parkinson's disease; ss.
XX
OS Homo sapiens.

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XX PN WO200140251-A1.
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XX PF 01-DEC-2000; 2000WO-US032745.
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XX PR 02-DEC-1999; 99US-0168387P.
XX
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX PI Wei Y;
XX
XX DR WPI; 2001-441480/47.
XX DR P-PSDB; AAU04295.
XX
XX PT Nucleic acid encoding human transforming growth factor alpha III (TGFA),
XX PT useful for preventing, diagnosing and/or treating e.g. Cancer and
XX PT Parkinson's disease.
XX
XX PS Claim 1; Fig 1; 302pp; English.
XX
XX CC The sequence represents the coding sequence of human transforming growth
XX CC factor (TGF) alpha HIII. TGF alpha HIII nucleic acid and protein may be
XX CC used in the prevention, diagnosis and treatment of diseases associated
XX CC with inappropriate polypeptide expression, for example immune disorders
XX CC (e.g. multiple sclerosis, systemic lupus erythematosus and human immuno-
XX CC deficiency virus (HIV) infections), hyperproliferative disorders (e.g.
XX CC cancers and Gaucher's disease), cardiovascular diseases (e.g. Scimitar
XX CC syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis),
XX CC angiogenic disorders (e.g. corneal graft neovascularisation and diabetic

CC retinopathy), neurological disorders (e.g. Huntington's chorea,
CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
CC for promoting wound healing, regeneration and/or chemotaxis (full details
CC given in specification). Additionally, the nucleic acid may be used to
CC produce the secreted polypeptides, by inserting the nucleic acids into a
CC host cell and culturing the cell to express the protein. It may also be
CC used as a DNA probe in diagnostic assays to detect and quantitate the
CC presence of similar nucleic acid sequences in samples, and therefore
CC which patients may be in need of restorative therapy. The polypeptides
CC may also be used as antigens in the production of antibodies against TGF
CC alpha HIII and in assays to identify modulators of TGF alpha HIII. The
CC anti-TGF alpha HIII antibodies may also be used as diagnostic agents for
CC detecting the presence of TGF alpha HIII in samples (e.g. by enzyme
CC linked immunosorbent assay (ELISA))
XX

SQ Sequence 923 BP; 235 A; 240 C; 210 G; 238 T; 0 U; 0 Other;

Query Match 72.2%; Score 353; DB 4; Length 923;
Best Local Similarity 84.0%; Pred. No. 3.4e-103;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGTGTCCAAACCTTTTACAGGCTT 62
Db 222 TGGGCTGGATCTCCAGAACTGTTCTCTGAGGACCTGTGTCCAAACCTTTTACAGGCTT 281
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAAAATCCTCTCAAGGATGATTTGGCCAAACCT 122
Db 282 ATACCACTGTATCATAGACCTTCAGGCAAAACCCCTCAAAGGTGACTTGGCCAAACCT 341
QY 123 TCCGTGGTTTACTCAGCTGCAGACTCTGATCTACTTACCACAGATGTTCCCTGCTCGGAG 182
Db 342 TCCGTGGCTTTACTCAGCTGCAGACTCTGATCTGTCACCAACATGTCAACTGCTCTGGAG 401
QY 183 GTAGTAATGCTGGGACAATGTTACTTCTTTCAAGGACAAGCAGATTTGCCAAGGGCAAA 242
Db 402 GATTAATGCTGGAACTATCTACCTCTTATATAGACACCAATCTGTCAAGGGCAAA 461
QY 243 GGGACCTTTGCAATAGCACTGGAAAGCCAGAAATGTCTCTGAGACGGATCTTGTGAT 302
Db 462 AGAACCTTTGCAATAACACTGGGACCCAGAAATGTCTCTGAGATGGATCTTGTGTAC 521
QY 303 CTGACGGTCTGTGGTCTTTTTCAGTGGCTTTGTGCTGATGTTTCCATGGATACAAAGTGA 362
Db 522 CTGATGTTCAGGTCTTTTTCAGTGGTGTGCTGATGTTTCCATGGATACAAAGTGA 581
QY 363 TGAGGCAAGGCTCAATTTTCACTGCTTATGTTCTTGGGATTTCCACCAACGCTAG 422
Db 582 TCGCCAGGCTCGTTCTCTCACTGCTTATGTTCTTGGGATTTCCGAGATTCGGAGCCACCTAT 641
QY 423 CCATCTNCATTTACTTTGGGACCCAGCGCGGAAAGCCAAAGCTTATGAGCCAC 482
Db 642 CCGTCTCCATTTCTGCTTTGGGACCCAGCGCGGAAAGCCAAAGCTTATGAGCTAT 701
QY 483 AAGACTT 489
Db 702 AGGTCTT 708

RESULT 4
ID ABA92166 standard; cDNA; 923 BP.
XX
AC ABA92166;
XX

DT 06-JUN-2002 (first entry)
XX
DE Human transforming growth factor alpha HIII cDNA.
XX
KW Transforming growth factor alpha HIII; TGF alpha HIII; human;
KW antiinflammatory; anticancer; vulnery; ophthalmological;
KW neuroprotective; antipsoriatic; gene therapy; diagnosis; gene; ss.
XX
OS Homo sapiens.

```

XX FH Key Location/Qualifiers
XX FT CDS 5..694 /*tag= a
XX FT /product= "TGF_alpha_HIII"
XX FT sig_peptide 5..79 /*tag= b
XX FT mat_peptide 80..691 /*tag= c
XX DN US2002025553-A1.
XX PD 28-FEB-2002.
XX PF 01-DEC-2000; 2000US-00726348.
XX PR 04-JAN-1996; 96US-0011136P.
XX PR 03-JAN-1997; 97US-00778545.
XX PR 02-DEC-1999; 99US-0168387P.
XX PA (WEIY/) WEI Y.
XX PI Wei Y;
XX DR WPI; 2002-280092/32.
XX DR P-PSDB; AAM51083.
XX FT Isolated nucleic acid molecule encoding Transforming Growth Factor alpha
XX FT HIII is used in preventing, treating or ameliorating a medical condition
XX FT e.g. cardiovascular or autoimmune diseases.
XX PS Claim 1; Fig 1A-B; 118pp; English.
XX CC The present sequence is that of cDNA (ATCC 97342) encoding human
XX CC transforming growth factor alpha HIII (TGF alpha HIII, see AAM51083), a
XX CC novel member of the TGF family. The cDNA was discovered in a human testis
XX CC cDNA library. The invention provides TGF alpha HIII nucleic acid
XX CC molecules (including those comprising sequential deletions from either
XX CC end of the present sequence) and polypeptides, vectors, host cells,
XX CC antibodies and recombinant methods for producing the polypeptides. The
XX CC TGF alpha HIII polypeptides and polynucleotides can be used in diagnostic
XX CC methods for detecting disorders related to TGF alpha HIII, and also for
XX CC therapeutic purposes, e.g. to stimulate wound healing to restore normal
XX CC neurological functioning after trauma or AIDS dementia, to treat ocular
XX CC disorders, to target certain cells, to treat kidney and liver disorders,
XX CC to promote hair follicular development, to stimulate angiogenesis for the
XX CC treatment of burns, ulcers and corneal incisions, and to stimulate
XX CC embryogenesis. Autoimmune diseases, disorders of haematopoietic cells,
XX CC allergic reactions, cardiovascular diseases, organ rejection,
XX CC inflammation, and hyperproliferative disorders may also be treated e.g.
XX CC by gene therapy. Methods are also provided for identifying agonists and
XX CC antagonists of TGF alpha HIII. Antagonists may be used to inhibit the
XX CC action of TGF alpha HIII polypeptides in the treatment of corneal
XX CC inflammation, neoplasia such as tumours and cancers, and psoriasis
XX SQ Sequence 923 BP; 235 A; 240 C; 210 G; 238 T; 0 U; 0 Other;

Query Match 72.2%; Score 353; DB 6; Length 923;
Best Local Similarity 84.0%; Pred No. 3.4e-103;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

Qy 4 TGAGGCTAGATCTTCAGAACTGTTCCT-CAGGATCTCTGTCACAACTTTTACAGGCTT 62
Db 222 TGGGGCTGGATCTCCAGAACTGTTCCTCTGAGGACCCCTGTCACAACTTTTACAGGCTT 281
Qy 63 ATACTGTATATATACAGCTTCAGCAATCTCTCAGGATGATTTGGCCAAACACCT 122
Db 282 ATACCACTGTATATACAGCTTCAGCAATCTCTCAGGATGATTTGGCCAAACACCT 341
Qy 123 TCCGTGGGTTTACTCAGCTCAGACTCTGATACCTACCAAGATGTTTCCCTGCTCGGAG 182
Db 342 TCCGTGGGTTTACTCAGCTCAGACTCTGATACCTACCAAGATGTTTCCCTGCTCGGAG 401

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QY 183 GTAGTAATGCTCTGGGACAAATCTTACTTTTTCATAGGCAACAGCAGATTGCGAAGGCAAA 242
Db 402 GAAATTAATGCTGGGAATACTATACCTCTTATATAGACAACCAAAATCTGTCAAGGGCAAA 461
QY 243 GGGACCTTTGCAATAGCACTGGAAGCCCGAAGTGTCTCTGAGAACGGATCTTTGTGCAT 302
Db 462 AGAACCTTTGCAATAGCACTGGAAGCCCGAAGTGTCTCTGAGAACGGATCTTTGTGTAC 521
QY 303 CTGACGGTCTCTGGTCTTTTTCAGTGCCTTTTGTGCTGATGTTTCCATGGATACAAAGTGA 362
Db 522 CTGATGGTCCAGGCTTTTTCAGTGTGTTTGTGCTGATGTTTCCATGGATACAAAGTGA 581
QY 363 TGAGGCAGGGCTCATTTTCACTGCTTATATGTTCTTTGGATCTCGGATCCACCAAGCTAG 422
Db 582 TGCGCCAGGGCTCGTCTCTCACTGCTTATGTTCTTTGGGATCTCGGAGCCACCACTTAT 641
QY 423 CCATCTNCATTTCTACTTTTGGGGAACCCAGAGCCCGGAAAGCCAAAGCTTATAGAGCCAC 482
Db 642 CCGTCTCCATTTCTGCTTTGGCGACCCAGCCGCGGAAAGCCAAAGCTTATAGAGCTTAT 701
QY 483 AAGACTT 489
Db 702 AGGTCTT 708

RESULT 5
AAX28432
ID AAX28432 standard; DNA; 932 BP.
XX AC AAX28432;
XX DT 22-JUN-1999 (first entry)
XX DE EGF-like homologue PRO240 coding sequence.
XX KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
XX KW EBAF-2; inhibitor; tumour growth; cancer; EGF-like homologue;
XX KW FGF-8 homologue; ss.
XX OS Homo sapiens.
XX PN WO9914327-A2.
XX PD 25-MAR-1999.
XX PF 10-SEP-1998; 98WO-US018824.
XX PR 17-SEP-1997; 97US-0059114P.
XX PR 17-SEP-1997; 97US-0059117P.
XX PR 18-SEP-1997; 97US-0059263P.
XX PR 15-OCT-1997; 97US-0062125P.
XX PR 17-OCT-1997; 97US-0062285P.
XX PR 17-OCT-1997; 97US-0062287P.
XX PR 24-OCT-1997; 97US-0062816P.
XX PR 29-OCT-1997; 97US-0063704P.
XX PR 25-NOV-1997; 97US-0066840P.
XX (GETH ) GENENTECH INC.
XX Botstein D, Goddard A, Gurney A, Hillan K, Lawrence DA, Roy M;
XX Wood WI;
XX WPI; 1999-229532/19.
XX DR P-PSDB; AAY05282.
XX PT Antibodies against specific proteins overexpressed in tumors.
XX Example 1; Fig 11; 130pp; English.
XX CC This sequence encodes the EGF-like homologue PRO240. The invention
XX CC relates to antibodies (Ab) that bind to any of the polypeptides (I)
XX CC designated PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246
XX CC or EBAF-2. The Ab, or other agents that inhibit expression and/or

```


QY 423 CCATCTNCACTTCTACTTTGGGAAACCCAGCGCCGAAAGCCAGGCTTATGAGCCAC 482
DB 649 CGGTCTCCATCTGCTTTGGGCGACCCAGCGCCGAAAGCCAGGCTTATGAGCCAC 708
QY 483 AAGACTT 489
DB 709 AGGTCTT 715

RESULT 8
AAC91553
ID AAC91553 standard; cDNA; 932 BP.
XX
AC AAC91553;
XX
DT 21-MAR-2001 (first entry)
XX
DE Human PRO240 cDNA.
XX
KW Human; PRO; cytostatic; neurotropic; neuroprotective; respiratory general;
KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW PRO agonist; cancer; inflammatory disorder; immunological disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200073348-A2.
XX
PD 07-DEC-2000.
XX
PF 30-MAY-2000; 2000WO-US014941.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 29-OCT-1999; 99US-0162506P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US0003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 02-MAR-2000; 2000WO-US004342.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
XX
PA (GETH) GENENTECH INC.
XX
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX
XX WPI; 2001-016509/02.
DR P-PSDB; AAB50951.
XX
XX Twenty eight nucleic acids encoding PRO polypeptides which are useful for
PT treating various tumors, e.g. breast cancer, and other inflammatory,
PT angiogenic and immunological disorders.
XX
XX Claim 20; Fig 1; 188pp; English.
XX
XX The present sequence is one of twenty eight nucleic acids encoding PRO
CC polypeptides. The PRO polypeptides and their agonists, including
CC antibodies, peptides, and small molecule agonists, may be used to treat

CC various tumours, e.g., cancers such as breast cancer, ovarian cancer,
CC renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung
CC cancer, bladder cancer, central nervous system cancer, melanoma or
CC leukaemia. They are also useful for treating other disorders such as
CC neuronal, glial, astrocytal, hypothalamic and other glandular
CC macrophagal, epithelial, stromal and blastocoeleic disorders, and
CC inflammatory, angiogenic and immunological disorders
XX

Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;

Query Match 72.2%; Score 353; DB 4; Length 932;
Best Local Similarity 84.0%; Pred. No. 3.4e-103;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTCTGTCACAACTTTTACAGGCTT 62
DB 229 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTCTGTCACAACTTTTATCATCAGGCAC 288
QY 63 ATACTGCTATTATCATAGACTTCAGGCAATCTCTCAGGATGATTTGCGCAACACCT 122
DB 289 ATACCACTGTCTATAGACTCTGCAAGCAACCCCTCAAAGTGACTTGGCCAAACCT 348
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACTACCAAGATGTTCCCTGTCTGGAG 182
DB 349 TCCGTGGCTTTACTCAGCTCCAGACTCTGATCTGTCACCAACATGTCACCTGTCTGGAG 408
QY 183 GTAGTAATGCTGGGCAATGTTACTTCTTCAAGNACAGCAGATTTGCCAGGGGAAA 242
DB 409 GAATTAATGCTGGATACTATCACTCTTATAGACAAACCAATCTGCAAGGGGAAA 468
QY 243 GGGACCTTTGCAATAGCACTGGAAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCAT 302
DB 469 AGAACCTTTGCAATAACACTGGGACCCAGAAATGTCTCTGAGATGGATCTTGTGTAC 528
QY 303 CTGACGCTCTGGTCTTTTTCAGTGGCTTTGCTGCTGATGTTTCCATGGATACAAGTGA 362
DB 529 CTGATGCTCCAGTCTTTTTCAGTGGTGTGCTGCTGATGTTTCCATGGATACAAGTGA 588
QY 363 TGAGGAGGCTCATTTTCACTGCTTATGTTTGGGATCTGGGATCCACACGCTAG 422
DB 589 TGCCAGGGCTGTTCTCACTGTTATGTTCTGGGATCTGGGAGCCACCTCTAT 648
QY 423 CCATCTNCACTTCTACTTTGGGAAACCCAGCGCCGAAAGCCAGGCTTATGAGCCAC 482
DB 649 CCGTCTCCATCTGCTTTGGGCGACCCAGCGCCGAAAGCCAGGCTTATGAGCTACAT 708
QY 483 AAGACTT 489
DB 709 AGGTCTT 715

RESULT 9

AAC91553
ID AAC91553 standard; cDNA; 932 BP.

XX AAC91553;

XX 30-APR-2001 (first entry)

XX Human cDNA encoding PRO240.

XX PRO240; UNQ214; human; immune disease; autoimmune disease; antirheumatic;
KW antiarthritic; antiinflammatory; antianemic; immunosuppressive;
KW antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide;
KW dermatological; antipsoriatic; antiallergic; antiallergic;
KW immunostimulant; serrate; lung cancer; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 12..701

XX FT /*tag= a

XX sig_peptide 12..101

```
mat_peptide
/*tag= b
102.698
/*tag= c
```

WO200105972-A1.

25-JAN-2001.

15-MAR-2000: 2000WO-US006884.

20-JUL-1999: 99US-0144758P.

(GETH) GENENTECH INC.

Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ;
Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D;
Watanabe CK, Wood WI;

WPI; 2001-103149/11.

P-PSDB; AAB20112.

New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes.

Claim 21: Fig 9: 127pp; English.

The present sequence is that of cDNA clone DNA34387-1138 (ATCC 209260) encoding novel human immunomodulator protein PRO240 (UNQ214) (see AAB20112). The clone was isolated from a foetal liver tissue cDNA library. The predicted protein (25 kDa, pI 7.83) shows homology to Drosophila serrate precursor and chicken C-serrate-1. Expression was observed in lung cancer, 8 squamous carcinomas and in 6/8 adenocarcinomas, in situ and infiltrating components. The invention provides polynucleotides (see AAF30050-62) encoding novel human PRO proteins (see AAB20108-20) including PRO240. Claimed compositions comprising these proteins or their agonists are useful for increasing infiltration of inflammatory cells into a tissue of a mammal, stimulating or enhancing an immune response in a mammal, or increasing the proliferation of T-lymphocytes in a mammal in response to an antigen. Claimed compositions comprising the PRO polypeptide or its antagonist have the opposite effect. A claimed method for treating an immune related disorder, such as a T cell disorder, involves administering the PRO polypeptide, an agonist antibody or an antagonist antibody. The disorder is selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthritis, systemic sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinated diseases (such as multiple sclerosis), autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's disease, (auto)immune-mediated skin diseases (such as bullous skin disease, erythema multiforme and psoriasis), allergic diseases (such as asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunologic diseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host disease) (all claimed). Claimed methods of diagnosing these disorders comprise detecting the level of expression of the PRO gene. Also claimed are a method of identifying a compound capable of inhibiting the expression or activity of the PRO polypeptide, vectors, host cells, antibodies and a method of stimulating an immune response by administering PRO240.

Sequence 932 BP: 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;

Query Match 72.2%; Score 353; DB 4; Length 932;
Best Local Similarity 84.0%; Pred. NO. 3.4e-103;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

4 TGAGGCTAGATCTTTCAGAACTGTCCCT-GAGGATCCTGGTCCAAACTTTTACAGGCTT 62

Db	229	TGGGGCTGGATCTCCAGAACTGTTTCTCTGGAGGACCTGGTCCAAACTTTTCATCAGGCAC	288
QY	63	ATATGCTATTATCATAGACCTTCAGGCAAAATCCTCTCAAGAGATGATTTGGGCCAAACACCT	122
Db	289	ATACCACTGTTCATCATAGACCTGCAAGCAAAACCCCTCRAAGGTGACTTTGGCCAAACACCT	348
QY	123	TCCGTGGGTTTACTCAGCTCAGTCGAGACTCTGATACTTACCAAGAGATGTTCCCTGTCTCTGGAG	182
Db	349	TCCGTGGGTTTACTCAGCTCAGACTCTGATCTGTCACCAACATGTCAACTGTCTCTGGAG	408
QY	183	GTAGTAATGCTCTGGGCAAAATGTTACTTTTCAAGGACCAAGCAGATTTGCCAAGGGCAAA	242
Db	409	GAATTAATGCTGGAATACTATCACCTCTTATATAGCAACCAAACTCTGTCAAGGGCAAA	468
QY	243	GGGACCTTTGCAATAGCACTGGAAGCCGAGAAATGTCTCTGAGAACGGATCTTGTGCAT	302
Db	469	AGAACCTTTGCAATAACACACTGGGAGCCGAGAAATGTCTCTGAGAATGGATCTTTGTGTAC	528
QY	303	CTGACGGTCCCTGGTCTTTTTCAGTGCCTTTTGTGCTGATGGTTTCCCATGGATACAAGTGA	362
Db	529	CTGATGGTCCAGGTCTTTTTCAGTGTGTTTGTGCTGATGGTTTCCCATGGATACAAGTGA	588
QY	363	TGAGCAGGGCTCAATTTTTCATCTGCTTAATGTTCTTTTGGGATCTTGGGATCAACACGCTAG	422
Db	589	TGCGCCAGGGCTCGTTTCTCACTGCTTATGTTTCTTGGGATTTCTGGGAGCCACCACTCTAT	648
QY	423	CCATCTCATTTCTACTTTTGGGAAACCCAGCGCCGAAAGCCAAAGGCTTTCATGAGCCACAC	482
Db	649	CGGCTTCATTTCTGCTTTGGGACCCAGCGCCGAAAGCCAAAGGCTTTCATGAGCTTACAT	708
QY	483	AAGACTT 489	
Db	709	AGGCTT 715	
RESULT 10			
AA	AAF60356	AAF60356 standard; cDNA; 932 BP.	
AC	AAF60356;		
XX	27-APR-2001 (first entry)		
XX	PRO240 coding sequence.		
DE	Cytostatic; PRO protein; tumour; cancer; ss.		
KW	Homo sapiens.		
XX	WO200105836-A1.		
XX	25-JAN-2001.		
XX	20-DEC-1999; 99WO-US030999.		
XX	20-JUL-1999; 99US-0144758P.		
PR	26-JUL-1999; 99US-0145698P.		
PR	08-SEP-1999; 99WO-US020594.		
PR	13-SEP-1999; 99WO-US020944.		
PR	15-SEP-1999; 99WO-US021090.		
PR	05-OCT-1999; 99WO-US023089.		
PR	29-NOV-1999; 99WO-US028214.		
PR	30-NOV-1999; 99WO-US028313.		
PR	02-DEC-1999; 99WO-US028564.		
XX	(GETH) GENENTECH INC.		
XX	Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI;		
PI	WPI; 2001-091968/10.		
DR	P-PSDB; AAB68595.		
XX	New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,		

PT useful for diagnosing and treating cancers.
PS Claim 50; Fig 7; 196pp; English.
XX
CC The present invention relates to PRO proteins and coding sequences. The
CC present sequence is the coding sequence for one such PRO protein. It was
CC found that the PRO genes are amplified in the genome of tumour cells. The
CC gene amplification is expected to be associated with the overexpression
CC of the gene product and contributes to tumourigenesis. Therefore,
CC antagonists of PRO proteins are useful for the treatment of benign or
CC malignant tumours, leukaemias, lymphoid malignancies and other disorders
CC such as neuronal, gliial, astrocytal, hypothalamic, glandular, epithelial,
CC inflammatory and immunologic disorders
XX
SQ Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;
Query Match 72.2%; Score 353; DB 4; Length 932;
Best Local Similarity 84.0%; Pred. No. 3.4e-103;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGTGTCACAACTTTTACAGGCTT 62
Db 229 TGGGGCTGATCTCCAGAACTGTTCTCTGGAGGACCTGTTCCAACTTTCATCAGGCAC 288
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCACACCT 122
Db 289 ATACCACTGTCATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCACACCT 348
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATATCTACCAAGATGTTCCCTGCTCGGAG 182
Db 349 TCCGTGGCTTTACTCAGCTCCAGACTCTGATATCTGCCACAACTGTCACACTGCTCGAG 408
QY 183 GTAGTAATCCCTGGGCAATGTTACTCTTTTCAAGCAAGCAGATTTGCCAAGGGCAAA 242
Db 409 GAATTAATCCCTGGGCAATGTTACTCTTTTCAAGCAAGCAGATTTGCCAAGGGCAAA 468
QY 243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCCTGAGAACGATCTTGTGCAT 302
Db 469 AGAACCTTTGCAATAGCACTGGAAGCCAGAAATGTCCTGAGAACGATCTTGTGCAT 528
QY 303 CTGACGGTCTCGTCTTTTSCAGTGGTGTGCTGATGTTTCCATGATACAAAGTGTGA 362
Db 529 CTGATGGTCCAGTCTTTTSCAGTGGTGTGCTGATGTTTCCATGATACAAAGTGTGA 588
QY 363 TGAGGAGGGCTCATTTTCACTGCTATGTTCTTTGGGATCTGGGATCCACAGCTAG 422
Db 589 TCGGCCAGGGCTCGTTCTCACTGCTATGTTCTTGGGATCTGGGATCCACACTCTAT 648
QY 423 CCATCTNCAATCTTACTTTGGGAAACCCAGCGCGGAAAGCCCAAGGCTTATGAGCCAC 482
Db 649 CCGTCTCCATTTGCTTTGGGACCCAGCGCGGAAAGCCCAAGGCTTATGAGCCAC 708
QY 483 AAGACTT 489
Db 709 AGTCTT 715
RESULT 11
ID ABK69964 standard; DNA; 932 BP.
XX
AC ABK69964;
XX
DT 15-JUL-2002 (first entry)
XX
DE cDNA encoding human Pro peptide #4.
XX
KW Human; ss; gene; PRO; secreted protein; transmembrane protein;
KW genetic disorder; tumour; cancer.
XX
OS Homo sapiens.
XX
PN WO200224888-A2.

XX
PD 28-MAR-2002.
XX
PF 29-AUG-2001; 2001WO-US027099.
XX
XX 01-SEP-2000; 2000US-0229896P.
PR 02-SEP-2000; 2000US-0230621P.
PR 22-SEP-2000; 2000US-0235147P.
PR 10-NOV-2000; 2000WO-US030873.
PR 12-JAN-2001; 2001US-0261878P.
PR 16-JAN-2001; 2001US-0261910P.
PR 16-JAN-2001; 2001US-0261939P.
PR 16-JAN-2001; 2001US-0262150P.
PR 25-JAN-2001; 2001US-0264395P.
PR 02-FEB-2001; 2001US-0266421P.
PR 28-FEB-2001; 2001US-0267623P.
PR 09-MAR-2001; 2001WO-US006520.
PR 03-APR-2001; 2001US-0274399P.
PR 04-APR-2001; 2001US-0280982P.
PR 04-APR-2001; 2001US-0282129P.
PR 04-APR-2001; 2001US-0282199P.
PR 05-MAY-2001; 2001US-0290589P.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
XX
(GETH) GENENTECH INC.
PA Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC,
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX WPI; 2002-362426/39.
DR P-PSDB; ABG34033.
XX
XX New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or for
PT genetic analysis of individuals with genetic disorders.
XX Claim 2; Fig 7; 218pp; English.
CC This invention relates to the cDNA and protein sequences of novel
CC secreted and transmembrane polypeptides PRO polypeptides. The invention
CC also comprises a method for producing the proteins of the invention by
CC recombinant means and antibodies specific for the protein of the
CC invention. The antibody may be used for detecting the PRO proteins of the
CC invention and may be used to modify their activity. polynucleotides may
CC be used as hybridisation probes for a cDNA library to isolate the full-
CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
CC probes for mapping the gene which encodes that PRO and for genetic
CC analysis of individuals with genetic disorders, in assays to identify
CC other proteins or molecules involved in binding reaction, to generate
CC transgenic animals or knock-out animals which in turn are useful in the
CC development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. The PRO polypeptides are
CC useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The sequences may also be used to detect
CC overexpression on PRO polypeptides in cancerous tumours and for screening
CC for differentially expressed genes using microarray technology. The
CC present sequence represents a cDNA encoding a human PRO protein of the
XX invention
XX
SQ Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;
Query Match 72.2%; Score 353; DB 6; Length 932;
Best Local Similarity 84.0%; Pred. No. 3.4e-103;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGTGTCACAACTTTTACAGGCTT 62
Db 229 TGGGGCTGATCTCCAGAACTGTTCTCTGGAGGACCTGTTCCAACTTTCATCAGGCAC 288

QY 63 ATACTGCTATTATCATAGACTTCAGCAAACTCTCTCAAGGATGATTTGGCCAAACACT 122
DB 289 ATACCACTGTCACTAGACTGCAAGCAAACTCTCAAGGATGATTTGGCCAAACACT 348
QY 123 TCGGTGGTTTACTCAGCTCAGACTCTGATCTACCAAGATGTTCCCTGCTGGAG 182
DB 349 TCGGTGGTTTACTCAGCTCAGACTCTGATCTACCAAGATGTTCCCTGCTGGAG 408
QY 183 GTAGTATGCTGGCAAGTTACTTCTTTCAGGACAGCAGATTTCCAGGGGCAA 242
DB 409 GAATTAAGCTGATATCTATCACTCTTATAGACACCAAACTCTGCAAGGGCAA 468
QY 243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTTCTGTGAGAACGGATCTTGTGCAT 302
DB 469 AGAACCTTTGCAATAGCACTGGAAGCCAGAAATGTTCTGTGAGAACGGATCTTGTGTAC 528
QY 303 CTGACGGTCTGCTTTTTCAGTGGCTTTTCTGCTGATGCTTTCCATGGATCAAGTGA 362
DB 529 CTGATGCTCAGGCTTTTTCAGTGGCTTTTCTGCTGATGCTTTCCATGGATCAAGTGA 588
QY 363 TGAGGACGGCTCATTTTCACTGTTATGTTCTTTTGGGATCTGGGATCCACCACGCTAG 422
DB 589 TGCGCAGGCTGCTTCTCACTGTTATGTTCTTTGGGATCTGGGATCCACCACGCTAT 648
QY 423 CCATCTNCATCTACTTTGGGGAACCCAGCGCGGAAAGCCAGGCTTATGAGCCACAC 482
DB 649 CCGTCTCCATCTGCTTTGGGGAACCCAGCGCGGAAAGCCAGGCTTATGAGCACTACAT 708
QY 483 AAGACTT 489
DB 709 AGGTCTT 715
RESULT 12
ACAS7990
ID ACA57990 standard; cdna; 932 BP.
AC ACA57990;
XX
XX
DT 09-JUN-2003 (first entry)
XX
DE cDNA encoding human neoplasia inhibiting PRO polypeptide PRO240.
XX
XX Human; ss; gene; tumour; cancer; neoplasia; liver cancer; sarcoma;
KW breast cancer; ovarian cancer; renal cancer; colorectal cancer; melanoma;
KW uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;
KW gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;
KW central nervous system cancer; hepatic carcinoma; glioblastoma;
KW neuronal disorder; glial disorder; astrocytal disorder;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoelic disorder;
KW inflammatory disorder; angiogenic disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
XX
FN US2002192209-A1.
XX
PD 19-DEC-2002.
XX
XX 30-NOV-2001; 2001US-00001054.
XX
XX 17-SEP-1997; 97US-0059114P.
PR 27-MAR-1998; 98US-0079689P.
PR 30-MAR-1998; 98US-0079920P.
PR 24-APR-1998; 98US-008299P.
PR 29-APR-1998; 98US-0083545P.
PR 12-MAY-1998; 98US-0085149P.
PR 02-JUN-1998; 98US-0087607P.
PR 11-JUN-1998; 98US-0088858P.
PR 25-JUN-1998; 98US-0090691P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98US-0099803P.
PR 14-SEP-1998; 98US-0100263P.
PR 15-SEP-1998; 98US-0100380P.
PR 23-SEP-1998; 98US-0101476P.
PR 10-NOV-1998; 98US-0107783P.
PR 18-NOV-1998; 98US-0108849P.
PR 19-NOV-1998; 98US-01180997.
PR 15-DEC-1998; 98US-0112420P.
PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98US-0115554P.
PR 12-JAN-1999; 98US-0115558P.
PR 12-JAN-1999; 98US-0115558P.
PR 20-JAN-1999; 98US-0116533P.
PR 08-MAR-1999; 98US-0116533P.
PR 10-MAR-1999; 98US-0123618P.
PR 12-APR-1999; 98US-00284291.
PR 20-APR-1999; 98US-00284291.
PR 27-APR-1999; 98US-0131294P.
PR 02-JUN-1999; 98US-0131294P.
PR 22-JUN-1999; 98US-0140650P.
PR 23-JUN-1999; 98US-0140650P.
PR 20-JUL-1999; 98US-0144758P.
PR 25-AUG-1999; 98US-00380137.
PR 25-AUG-1999; 98US-00380137.
PR 25-AUG-1999; 98US-00380137.
PR 01-SEP-1999; 98US-00380137.
PR 01-SEP-1999; 98US-00380137.
PR 08-SEP-1999; 98US-00380137.
PR 18-OCT-1999; 98US-00403297.
PR 29-OCT-1999; 98US-0142506P.
PR 10-NOV-1999; 98US-00423741.
PR 30-NOV-1999; 98US-00423741.
PR 01-DEC-1999; 98US-00423741.
PR 02-DEC-1999; 98US-00423741.
PR 09-DEC-1999; 98US-0170262P.
PR 16-DEC-1999; 98US-0170262P.
PR 20-DEC-1999; 98US-0170262P.
PR 06-JAN-2000; 98US-0170262P.
PR 11-FEB-2000; 98US-0170262P.
PR 18-FEB-2000; 98US-0170262P.
PR 18-FEB-2000; 98US-0170262P.
PR 02-MAR-2000; 98US-0170262P.
PR 03-MAR-2000; 98US-0170262P.
PR 15-MAR-2000; 98US-0170262P.
PR 30-MAR-2000; 98US-0170262P.
PR 17-MAY-2000; 98US-0170262P.
PR 22-MAY-2000; 98US-0170262P.
PR 30-MAY-2000; 98US-0170262P.
PR 02-JUN-2000; 98US-0170262P.
PR 11-AUG-2000; 98US-0170262P.
PR 23-AUG-2000; 98US-0170262P.
PR 23-AUG-2000; 98US-0170262P.
PR 10-NOV-2000; 98US-0170262P.
PR 10-NOV-2000; 98US-0170262P.
PR 28-FEB-2001; 98US-0170262P.
PR 01-MAR-2001; 98US-0170262P.
PR 09-MAR-2001; 98US-0170262P.
PR 25-MAY-2001; 98US-0170262P.
PR 25-MAY-2001; 98US-0170262P.
PR 01-JUN-2001; 98US-0170262P.
PR 01-JUN-2001; 98US-0170262P.
PR 14-JUN-2001; 98US-0170262P.
PR 20-JUN-2001; 98US-0170262P.
PR 29-JUN-2001; 98US-0170262P.
PR 09-JUL-2001; 98US-0170262P.
PR 30-JUL-2001; 98US-0170262P.
PR 06-AUG-2001; 98US-0170262P.
PR 09-AUG-2001; 98US-0170262P.
PR 13-AUG-2001; 98US-0170262P.
PR 28-AUG-2001; 98US-0170262P.
PR 29-AUG-2001; 98US-0170262P.

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PR 04-SEP-2001; 2001US-00946374.
XX (GETH ) GENENTECH INC.
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
XX Shelton DL, Smith V, Watanabe CK, Wood WI;
XX WPI; 2003-328851/06.
DR P-PSDB; ABU71416.
XX
XX Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
PT treating tumor, preferably cancer, or for treating neuronal, glial,
PT hypothalamic, stromal, inflammatory, angiogenic and immunologic
PT disorders.
XX
XX Claim 20; Fig 1; 186pp; English.
XX
XX The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its
CC associated signal peptide or PRO polypeptide extracellular domain with or
CC without its associated signal peptide. The PRO polypeptide or an antibody
CC binding to it is useful for inhibiting the growth of a tumor cell. A
CC composition containing a PRO polypeptide is useful for inhibiting
CC neoplastic cell growth or for treating a tumor, preferably cancer (such
CC as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC bladder, gastric, pancreatic, vulval, thyroid, central nervous system
CC cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or
CC leukaemia) in a mammal. The PRO polypeptide is useful for identifying its
CC agonists. The PRO polypeptide or an antibody binding to it is useful in
CC the preparation of a medicament for treating a condition which is
CC responsive to the PRO polypeptide or an antibody binding to it. The PRO
CC polypeptide or an antibody binding to it is also useful for treating
CC neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC epithelial, stromal, blastocytic, inflammatory, angiogenic and
CC immunologic disorders. The present sequence represents a cDNA encoding a
CC PRO polypeptides of the invention
XX
XX Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;
XX
XX Query Match 72.2%; Score 353; DB 7; Length 932;
XX Best Local Similarity 84.0%; Pred. No. 3.4e-103;
XX Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
XX
XX 4 TGAGGCTAGACTTTCAGAACTGTTCCTT-GAGGATCCTGGTCCAAACTTTTACAGGCTT 62
XX 229 TGGGGCTGATCTCCAGACTGTCTCTCGAGGACCTGTCTCAACTTTCATCAGGCAC 288
XX 63 ATACTGCTATTATCATAGACCTTTCAGGAAATCCTCTCAAGGATGATTTGGCCAACTCT 122
XX 289 ATACCACCTGTCATAGACCTTCAGCAAGCAAAACCCCTCAAGGTGCACTTGGCCAACT 348
XX 123 TCGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTCCTCTCTGGAG 182
XX 349 TCGTGGCTTTTACTCAGCTCCAGACTCTGATCTGCGACCAACATGTCAACTGCTGGAG 408
XX 183 GTAGTAATGCTGGGCAATGTACTTCTTTCAAGCAAGCAGATTTGCCAAGGGCAAA 242
XX 409 GAATTAATGCTGGAATCATCATCCTCTATATAGAACCAAACTCTGCAAGGGCAAA 468
XX 243 GGCACCTTGCATAGACCTGAGAGCCGAGAAATGTCTGAGACGATCTTGCTAT 302
XX 469 AGAACCTTTGCAATAACACTGGGGACCCAGAAATGTCTGAGATGATCTTGTGTAC 528
XX 303 CTACACGCTCTGCTCTTTTGCAGTGGGTTTGTCTGATGTTTCCATGATCAACAGTGTA 362
XX 529 CTGATGCTCAGGCTCTTTTGCAGTGTGTTGTCTGATGTTTCCATGATCAACAGTGTA 588
XX 363 TGAGGCAAGGCTCATTTTCTACTGCTTATGTTCTTTTGGGATCTGGGATCCACACGCTAG 422
XX 589 TGGCCAGGCGCTGCTTCTACTGCTTATGTTCTTGGGATTTCTGGGAGCCACCACTCTAT 648
XX 423 CCATCTNCATCTTACTTTGGGAAACCCAGCGCGGAAAGCCAAAGGCTTTCATGAGCCACAC 482
XX
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Db 649 CCGTCTCCATTCTGTTTGGGCGACCGCGCGAAGCCAAAGACTTTCATGAATACAT 708
Qy 483 AAGACTT 489
Db 709 AGGTCTT 715
RESULT 13
ID ADA01275 standard; cDNA; 932 BP.
XX ADA01275;
XX 06-NOV-2003 (first entry)\
XX Human PRO polynucleotide #4.
XX
XX Human; Gene; ss; secreted polypeptide; transmembrane polypeptide;
XX tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; tumour;
XX adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer;
XX microvascular endothelial cell; endothelial cell tube formation;
XX sports-related joint problem; articular cartilage defect; osteoarthritis;
XX rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.
XX
XX Homo sapiens.
XX
XX US2003068779-A1.
XX
XX 10-APR-2003.
XX
XX 16-SEP-2002; 2002US-00245107.
XX
XX 09-MAY-2001; 2001US-0230589P.
XX 29-AUG-2001; 2001WO-US027099.
XX 18-JUL-2002; 2002US-00197942.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Eaton DL, Filvaroff B, Goddard A, Grimaldi JC;
XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
XX Fong S;
XX WPI; 2003-625484/59.
XX P-PSDB; ADA01276.
XX
XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
XX stimulating proliferation of human microvascular endothelial cells, and
XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
XX cells.
XX
XX Claim 2; Fig 7; 307pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the polynucleotides encoding them. The
XX invention also relates to an antibody which specifically binds to a PRO
XX polypeptide, a method for stimulating the release of tumour necrosis
XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the
XX proliferation or differentiation of chondrocyte cells and a method for
XX detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
XX colon, breast, prostate, rectal, cervical and liver tumours). The
XX polynucleotides are useful in molecular biology, including uses as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA and in gene therapy. The polynucleotides may also
XX be used in preparing PRO polypeptides by recombinant techniques and in
XX generating either transgenic animals or knock-out animals which are
XX useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptides or antibodies are used in preparing a
XX medicament for treating a condition responsive to the polypeptides or
XX antibodies, such as tumours, for stimulating and inhibiting proliferation
XX of human microvascular endothelial cells, for inducing endothelial cell
XX tube formation and for treating sports-related joint problems, articular
XX cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
XX represents a human PRO polynucleotide of the invention.
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XX	Sequence	932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;	
XX	Query Match	72.2%; Score 353; DB 8; Length 932;	
XX	Best Local Similarity	84.0%; Pred. No. 3.4e-103;	
XX	Matches	409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;	
QY	4	TCAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGTGCCAACTTTTACAGGCTT 62	
DB	229	TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCTGTGCCAACTTTTCATCAGGCAC 288	
QY	63	ATACCTGTATTATCATAGACCTTCAGGCAAACTCTCAAGGATGATTGGCCCAACCT 122	
DB	289	ATACCACTGTCTATCATAGACCTTCAGCAAACTCTCAAGGATGATTGGCCCAACCT 348	
QY	123	TCCGTGGGTTTACTCAGCTGCAGACTCTGTATCTACCAAGATGTTCCCTGTCTCGAG 182	
DB	349	TCCGTGGGTTTACTCAGCTGCAGACTCTGTATCTACCAAGATGTTCCCTGTCTCGAG 408	
QY	183	GTAGTAATGCCTGGGCAATGTTACTTCTTCAGGGACAGACATTTGCCAGGGCAAA 242	
DB	409	GAATTAATGCCTGGGCAATGTTACTTCTTCAGGGACAGACATTTGCCAGGGCAAA 468	
QY	243	GGGACCTTTTGAATAGCACTGGAAAGCCAGAAATGTCTCTGAGAAGGATTTGTGCAT 302	
DB	469	AGAACCTTTTGAATAGCACTGGGAGCCAGAAATGTCTCTGAGAATGGAATCTGTATC 528	
QY	303	CTGACGGTCCCGCTTTTTCAGTGGCTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 362	
DB	529	CTGATGCTCAGGCTTTTTCAGTGGCTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588	
QY	363	TGAGGCGAGGCTCATTTTTCAGTGGCTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 422	
DB	589	TGCGCCAGGCTCGTTTCTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 648	
QY	423	CCATCTTCATTTCTACTTTTGGGACCCAGCGCCGGAAGCCAAAGCTTTCATGAGTACAT 482	
DB	649	CCGCTTCATTTCTGTTTGGGACCCAGCGCCGGAAGCCAAAGCTTTCATGAGTACAT 708	
QY	483	AAGACTT 489	
DB	709	AGGCTT 715	
RESULT 14	ADA43704	standard; cDNA; 932 BP.	
XX	ADA43704;		
XX	20-NOV-2003	(first entry)	
XX	Human cDNA encoding secreted/transmembrane polypeptide PRO240.		
DE	ss; gene; human; PRO; secreted protein; transmembrane protein;		
XX	endothelial cell tube formation; chondrocyte cell differentiation;		
KW	microvascular endothelial cell; tumour; lung tumour; colon tumour;		
KW	breast tumour; prostate tumour; rectal tumour; kidney tumour;		
KW	liver tumour; cytostatic; vaccine.		
XX	Homo sapiens.		
OS	US2003064474-A1.		
XX	03-APR-2003.		
XX	16-SEP-2002; 2002US-00245859.		
XX	29-AUG-2001; 2001WO-US027099.		
PR	18-JUL-2002; 2002US-00197942.		
XX	(GETH) GENENTECH INC.		

Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC, Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z, Fong S; WPI; 2003-605867/57. P-PSDB; ADA43705.

New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or PRO1383, useful in molecular biology, chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy.

Claim 2; Fig 7; 308pp; English.

The invention relates to an isolated secreted/transmembrane (PRO) polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the nucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide, an extracellular domain of PRO with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000, and PRO10275, PRO21207, or PRO34274 polypeptide or its agonist) and an oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptide is useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080 and PRO21383 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006 polypeptides are useful for inhibiting the proliferation of human microvascular endothelial cells. PRO polypeptides are useful for detecting the presence of tumour in a mammal, including tumours of lung, colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and PRO34274 polypeptides are useful for inducing endothelial cell tube formation. PRO or the antibody are useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acid is useful as a hybridisation probe, in chromosome and gene mapping, in the generation of antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence encodes a PRO protein.

XX SQ Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;

Query Match 72.2%; Score 353; DB 8; Length 932; Best Local Similarity 84.0%; Pred. No. 3.4e-103; Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TCAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTGTGCCAACTTTTACAGGCTT 62

DB 229 TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCTGTGCCAACTTTTCATCAGGCAC 288

QY 63 ATACCTGTATTATCATAGACCTTCAGGCAAACTCTCAAGGATGATTGGCCCAACCT 122

DB 289 ATACCACTGTCTATCATAGACCTTCAGCAAACTCTCAAGGATGATTGGCCCAACCT 348

QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGTATCTACCAAGATGTTCCCTGTCTCGAG 182

DB 349 TCCGTGGGTTTACTCAGCTGCAGACTCTGTATCTACCAAGATGTTCCCTGTCTCGAG 408

QY 183 GTAGTAATGCCTGGGCAATGTTACTTCTTCAGGGACAGACATTTGCCAGGGCAAA 242

DB 409 GAATTAATGCCTGGGCAATGTTACTTCTTCAGGGACAGACATTTGCCAGGGCAAA 468

QY 243 GGGACCTTTTGAATAGCACTGGAAAGCCAGAAATGTCTCTGAGAAGGATTTGTGCAT 302

DB 469 AGAACCTTTTGAATAGCACTGGGAGCCAGAAATGTCTCTGAGAATGGAATCTGTATC 528

QY 303 CTGACGGTCCCGCTTTTTCAGTGGCTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 362

DB 529 CTGATGCTCAGGCTTTTTCAGTGGCTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588

QY 363 TGAGGCGAGGCTCATTTTTCAGTGGCTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 422

DB 589 TGCGCCAGGCTCGTTTCTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 648

QY 423 CCATCTTCATTTCTACTTTTGGGACCCAGCGCCGGAAGCCAAAGCTTTCATGAGTACAT 482

DB 649 CCGCTTCATTTCTGTTTGGGACCCAGCGCCGGAAGCCAAAGCTTTCATGAGTACAT 708

QY 483 AAGACTT 489

DB 709 AGGCTT 715

RESULT 14

ADA43704

ADA43704 standard; cDNA; 932 BP.

XX ADA43704;

XX 20-NOV-2003 (first entry)

XX Human cDNA encoding secreted/transmembrane polypeptide PRO240.

DE ss; gene; human; PRO; secreted protein; transmembrane protein;

XX endothelial cell tube formation; chondrocyte cell differentiation;

KW microvascular endothelial cell; tumour; lung tumour; colon tumour;

KW breast tumour; prostate tumour; rectal tumour; kidney tumour;

KW liver tumour; cytostatic; vaccine.

XX Homo sapiens.

OS US2003064474-A1.

XX 03-APR-2003.

XX 16-SEP-2002; 2002US-00245859.

XX 29-AUG-2001; 2001WO-US027099.

PR 18-JUL-2002; 2002US-00197942.

XX (GETH) GENENTECH INC.

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Db 529 CTGATGGTCCAGGCTCTTTGCAAGTGTGTTGGCTGATGGTTTCCATGATACCAAGTGA 588
QY 363 TGAGGCAGGGCTCATTCTTCACTGCTTATGCTTTCTTTGGGATTCGGATCCACCAAGCTAG 422
Db 589 TCGGCAGGGCTCGTCTCAGCTGCTTATGCTTTCTTGGGATTCGGAGCCACCACTCTAT 648
QY 423 CCATCTNCAATTTACTTTGGGAAACCCAGCGCCGGAAGCCAAAGCTTATGAGCCACAC 482
Db 649 CCGTCTCCATTTCTGCTTTGGGCGCCAGCGCCGGAAGCCAAAGCTTATGAGCTATACAT 708
QY 483 AAGACTT 489
Db 709 AGGTCTT 715

RESULT 15
ADA43472
ID ADA43472 standard; cDNA; 932 BP.
XX AC ADA43472;
XX DT 20-NOV-2003 (first entry)
XX DE Human cDNA encoding secreted/transmembrane polypeptide PRO240.
XX SS; gene; human; PRO; secreted protein; transmembrane protein;
XX KW endothelial cell tube formation; chondrocyte cell differentiation;
XX KW microvascular endothelial cell; tumour; lung tumour; colon tumour;
XX KW breast tumour; prostate tumour; rectal tumour; kidney tumour;
XX KW liver tumour; cytostatic; vaccine.
XX OS Homo sapiens.
XX PN US2003073196-A1.
XX PD 17-APR-2003.
XX PF 18-SEP-2002; 2002US-00246210.
XX PR 04-APR-2001; 2001US-0282199P.
XX PR 29-AUG-2001; 2001WO-US027099.
XX PR 18-JUL-2002; 2002US-00197942.
XX PA (GETH ) GENENTECH INC.
XX PI Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
XX PI Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
XX PI Fong S;
XX DR WPI; 2003-743814/70.
XX DR P-PSDB; ADA43473.
XX PT New secreted and transmembrane PRO polypeptides, e.g. PRO20080 or
XX PT PRO21383 useful for stimulating the proliferation or differentiation of
XX PT chondrocyte cells and detecting the presence of a tumor in a mammal.
XX PS Claim 2; Fig 7; 307pp; English.
XX CC The invention relates to an isolated secreted/transmembrane (PRO)
XX CC polypeptide, having at least 80% sequence identity to a sequence selected
XX CC from any one of the 57 amino acid sequences given in specification, or to
XX CC a sequence encoded by a nucleic acid molecule selected from any one of
XX CC the nucleic acids deposited under any of the ATCC accession numbers given
XX CC in specification, or a sequence having at least 80% identity to PRO
XX CC lacking its associated signal peptide, an extracellular domain of PRO
XX CC with or without its associated signal peptide. Also included are vectors,
XX CC transformed host cells, anti-PRO antibodies, the nucleic acids encoding
XX CC PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
XX CC administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000,
XX CC PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and
XX CC an oligonucleotide probe derived from any one of the above nucleotide
XX CC sequences. PRO6018 polypeptide is useful for stimulating the
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CC proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080
CC and PRO21383 polypeptides are useful for stimulating the proliferation of
CC human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006
CC polypeptides are useful for inhibiting the proliferation of human
CC microvascular endothelial cells. PRO polypeptides are useful for
CC detecting the presence of tumour in a mammal, including tumours of lung,
CC colon, breast, prostate, rectal, kidney and liver. PRO381, PRO1560,
CC PRO189, PRO499, PRO6308, PRO6000, PRO1207, PRO20933 and
CC PRO34274 polypeptides are useful for inducing endothelial cell tube
CC formation. PRO or the antibody are useful in the preparation of a
CC medicament for treating a condition responsive to PRO polypeptide. The
CC oligonucleotide probes are useful for isolating genomic and cDNA
CC nucleotide sequences, for measuring or detecting the expression of an
CC associated gene, and as antisense probes. PRO nucleic acid is useful as a
CC hybridisation probe, in chromosome and gene mapping, in the generation of
CC antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and
CC PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The
XX present sequence encodes a PRO protein.
XX SQ Sequence 932 BP; 239 A; 241 C; 214 G; 237 T; 0 U; 1 Other;

Query Match 72.2%; Score 353; DB 8; Length 932;
Best Local Similarity 84.0%; Pred. No. 3.4e-103;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TGAGGCTAGATCTTCAGAACTGTTTCCTT-CAGGATCCTGTCACAACTTTTACAGGCTT 62
Db 229 TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTCACAACTTTTCAITCAGGCAC 288
QY 63 ATACTGCTATTATCATAGACTTCAGGCAAACTCTCAAGGATGATTTGGCCAAACCT 122
Db 289 ATACCACCTGTTCATCATAGACTGTCAGCAAAACCCCTCAAAGGTGACTTGGCCAAACCT 348
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGCTCTGGAG 182
Db 349 TCCGTGGCTTTACTCAGCTGCAGACTCTGATACCTGTCACCAACATGTCACACTGCTCTGGAG 408
QY 183 GTAGTAATGCTCTGGCAAACTGTTACTTCTTCAAGGACAAGCAGATTGCCCAGGGCAAA 242
Db 409 GAATTATGCTCTGGAATACTATCACTCTTATATAGACACCAAACTCTGTCAAGGGCAAA 468
QY 243 GGGACCTTTGCAATAGCACTGGAAAGCCAGAAATGTCCTCTGAGACGGATCTTGTGCAT 302
Db 469 AGAACCTTTGCAATAACACTGGGGACCCAGAAATGTGTCTGAGAATGGATCTTGTGTAC 528
QY 303 CTGACGGTCTGCTGCTTTTGGCAGTGCCTTGTGCTGATGTTTCCATGGATACAAAGTGA 362
Db 529 CTGATGCTCAGGCTCTTTTGGCAGTGTGTTGTGCTGATGTTTCCATGGATACAAAGTGA 588
QY 363 TGAGGCAGGGCTCATTCTTCACTGCTTATGCTTTTGGGATTTCTGGATTCACCAAGCTAG 422
Db 589 TCGCCAGGGCTCGTCTCTCACTGCTTATGTTCTTCCGGGATTTCTGGAGCCACCACTCTAT 648
QY 423 CCATCTNCAATTTACTTTGGGAAACCCAGCGCCGGAAGCCAAAGCTTATGAGCCACAC 482
Db 649 CCGTCTCCATTTCTGCTTTGGGCGCCAGCGCCGGAAGCCAAAGCTTATGAGCTATACAT 708
QY 483 AAGACTT 489
Db 709 AGGTCTT 715
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Search completed: June 25, 2004, 22:17:58
Job time : 727 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 21:55:07 ; Search time 1995 Seconds

(without alignments)
7319.602 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 489

Sequence: 1 gactgaggtagattcttag.....tnatgagccacacaagactt 489

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hrc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hrc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	487	99.6	489	29	CG539763 OST131079
2	476	97.3	486	29	CG615808 OST1307322
3	472	96.5	763	13	BUS57697 AGENCOURT
4	471.4	96.4	512	9	AA017836 mh44h03.r

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	471.4	96.4	762	14	CD364102
6	471.4	96.4	791	9	AU080019
7	471.4	96.4	838	14	CK128347
8	471.4	96.4	884	11	BC038336
9	469.8	96.1	933	11	AK002276
10	459.4	93.9	614	9	AA108529
11	458.6	93.8	754	12	BG142354
12	456.2	93.3	669	10	BE994240
13	449.2	91.9	635	29	CG589400
14	447.8	91.6	720	13	BQ748981
15	446.4	91.3	469	13	BX520494
16	445.4	91.1	671	9	AI116932
17	432.2	88.4	616	10	BE985460
18	432.2	88.4	640	14	CA452314
19	415.8	85.0	614	10	BF462535
20	412.2	84.3	475	9	AI115639
21	410.8	84.0	470	9	AA786965
22	397	81.2	724	13	BQ199079
23	395.4	80.9	425	9	AA450686
24	394.4	80.7	483	9	AA273740
25	394.4	80.7	1039	14	W15719
26	393	80.4	499	10	BE848379
27	382.4	78.2	566	10	AW908899
28	381.6	78.0	605	10	BE956564
29	378.4	77.4	637	13	BY744162
30	369.4	75.5	460	10	BE852127
31	369.4	75.0	592	9	AW044815
32	362	74.0	407	10	BE861531
33	359.2	73.5	983	10	BF568872
34	358	73.2	902	14	CF587266
35	354.6	72.5	551	13	BQ305549
36	353.8	72.4	1048	9	AL560711
37	353.6	72.3	836	13	BQ716341
38	353	72.2	561	13	BQ305554
39	353	72.2	566	13	BQ305557
40	353	72.2	582	13	BQ305556
41	353	72.2	590	13	BQ305551
42	353	72.2	591	10	AW912084
43	353	72.2	748	13	BUS40754
44	353	72.2	752	14	CB957744
45	353	72.2	758	12	BI760599

ALIGNMENTS

RESULT 1	CG539763	489 bp	DNA	linear	GSS 01-OCT-2003
CG539763	OST131079	Mus musculus 129Sv/Ev	Mus musculus genomic clone		
LOCUS	OST131079	genomic survey sequence.			
DEFINITION	CG539763	GI:37326335			
ACCESSION	CG539763				
VERSION	CG539763.1				
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 489)				
	Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C., Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T.				
	Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention				
	Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)				
	Contact: Zambrowicz BP				
	OmiBank				
	Lexicon Genetics Incorporated				
	4000 Research Forest Drive, The Woodlands, TX 77381, USA				

TITLE
JOURNAL
COMMENT

Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
 Location/Qualifiers

FEATURES

source
 1. 489
 /organism="Mus musculus"
 /mol_type="genomic DNA"
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 /db_xref="taxon:10090"
 /clone="OST131079"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129SV/Ev"

ORIGIN

Query Match 99.6%; Score 487; DB 29; Length 489;
 Best Local Similarity 100.0%; Pred. No. 6.5e-136;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GACTGAGCGCTAGATCTTCAGAACTGTTCCCTGAGGATCTGGTCCAAACTTTTACAGGC 60
 Db 1 GACTGAGCGCTAGATCTTCAGAACTGTTCCCTGAGGATCTGGTCCAAACTTTTACAGGC 60
 Qy 61 TTATAGCTATATATATATAGACCTTCAGGCAATCTCTCAAGGATGATTGGCCACAC 120
 Db 61 TTATAGCTATATATATAGACCTTCAGGCAATCTCTCAAGGATGATTGGCCACAC 120
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 Db 121 CTTCCGTTGGTTTACTCAGCTGCAGACTCTGATCTACCAAGAGTGTCCCTGTCTCTG 180
 Qy 181 AGTGTAGTAAGCTGGGACATGTTACTTCTTCAAGGACAAAGAGTTTGGCAAGGCA 240
 Db 181 AGTGTAGTAAGCTGGGACATGTTACTTCTTCAAGGACAAAGAGTTTGGCAAGGCA 240
 Qy 241 AAGGAGCTTTGCAATAGCACTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGC 300
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 Qy 301 ATCTGAGCGTCTGGTCTTTTGCAGTGGTTGTGTGATGGTTTCCATGGATACAAAGTG 360
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 Qy 361 TATGAGCAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGATCCACACGCT 420
 Db 361 TATGAGCAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGATCCACACGCT 420
 Qy 421 AGCCATCTNCACTTCTTTGGGAAACCCAGCGCCGGAAGCAAGGCTTATGAGCCAC 480
 Db 421 AGCCATCTNCACTTCTTTGGGAAACCCAGCGCCGGAAGCAAGGCTTATGAGCCAC 480
 Qy 481 ACAAGACTT 489
 Db 481 ACAAGACTT 489

CG615908 496 bp DNA linear GSS 02-OCT-2003
 OST307322 Mus musculus 129SV/Ev Mus musculus genomic clone
 LOCUS OST307322, genomic survey, sequence.
 CG615908
 CG615908.1 GI:37439757
 GSS.
 Mus musculus (house mouse)

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 496)
 Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
 Piggott, J., BeltrandeRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
 Fiddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,
 Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D.,

TITLE

JOURNAL

COMMENT

Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
 Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
 Zhu, Q., Person, C. and Sands, A.T.
 Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 Contact: Zambrowicz BP
 OmniBank
 Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
 Class: Gene Trap.
 Location/Qualifiers

FEATURES

source

1. 496
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 /mol_type="genomic DNA"
 /strain="129SV/Ev"
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 /clone="OST307322"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129SV/Ev"

ORIGIN

Query Match 97.3%; Score 476; DB 29; Length 496;
 Best Local Similarity 99.6%; Pred. No. 1.4e-132;
 Matches 476; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 12 GATCTTCAGAACTGTTCCCTGAGGATCTGGTCCAAACTTTTACAGCTTATCTGCTA 71
 Db 8 GATCTTCAGAACTGTTCCCTGAGGATCTGGTCCAAACTTTTACAGCTTATCTGCTA 67
 Qy 72 TTATCATAGACTTCAGGCAAAATCTCTCAAGGATGATTGGCCAAACACCTTCCGTGGT 131
 Db 68 TTATCATAGACTTCAGGCAAAATCTCTCAAGGATGATTGGCCAAACACCTTCCGTGGT 127
 Qy 132 TTACTCAGCTCAGACTCTGATCTACCAAGAGTGTCCCTGCTGGAGTAGTAATG 191
 Db 128 TTACTCAGCTCAGACTCTGATCTACCAAGAGTGTCCCTGCTGGAGTAGTAATG 187
 Qy 192 CTTGGGCAATGTTTACTTCTTCAAGGACAAAGAGATTTGCCAAGGGCAAGGACCTTT 251
 Db 188 CTTGGGCAATGTTTACTTCTTCAAGGACAAAGAGATTTGCCAAGGGCAAGGACCTTT 247
 Qy 252 GCATAGACCTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCATCTCAGCGTC 311
 Db 248 GCATAGACCTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCATCTCAGCGTC 307
 Qy 312 CTGCTCTTTTGCAGTGGCTTTGTGCTGATGTTTCCATGGATACAAAGTGTATGAGGAGG 371
 Db 308 CTGCTCTTTTGCAGTGGCTTTGTGCTGATGTTTCCATGGATACAAAGTGTATGAGGAGG 367
 Qy 372 GCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGGATCCACACGCTAGCCATCTNCA 431
 Db 368 GCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGGATCCACACGCTAGCCATCTCCA 427
 Qy 432 TTCTACTTTTGGGAAACCCAGCGCCGGAAGCAAGGCTTATGAGCCACCAAGACTT 489
 Db 428 TTCTACTTTTGGGAAACCCAGCGCCGGAAGCAAGGCTTATGAGCCACCAAGACTT 485

RESULT 3

BU557697

LOCUS

DEFINITION

AGENCY: 10187185 NIH MGC 144 Mus musculus cDNA clone

IMAGE: 6585654 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BU557697 763 bp mRNA linear EST 16-SEP-2002
 AGENCY: 10187185 NIH MGC 144 Mus musculus cDNA clone
 IMAGE: 6585654 5', mRNA sequence.
 BU557697 GI:22907993
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 763)
NIH-MGC <http://mgi.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2797 row: p column: 06
High quality sequence stop: 579.
Location/Qualifiers
1..763
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6585654"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH_MGC_144"
/note="Organ: Brain; Vector: pDNR-LIB; Site_1: Sfil
(ggccatgatggc); Site_2: Sfil (ggcgctcgcc); cDNA made
by oligo-dT priming and directionally cloned. 5' and 3'
adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGAGATGCGCATTCAGCGCGG-3' and
5'-ATTCAGAGCGCGCGCGACATG-dt(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the 0.2-0.5
kb size fraction (other fractions present in NIH_MGC_143).
Library created in the laboratory of M. Brownstein (NIMH,
NIH). Note: this is a NIH_MGC Library."

Query Match 96.5%; Score 472; DB 13; Length 763;
Best Local Similarity 99.4%; Pred. No. 2.8e-131;
Matches 483; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 5 GAGGCTAGATCTTCAGAACTGTTCCTG-AGGATCCTGTGTCACAACTTTTACAGGCTTA 63
DB 121 GAGGCTAGATCTTCAGAACTGTTCCTGAGAGATCTGTGTCACAACTTTTACAGGCTTA 180
QY 64 TACTGCTATATCATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACACCTT 123
DB 181 TACTGCTATATCATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACACCTT 240
QY 124 CCGTGGTGTACTCAGCTCAGACTCTGATACCTACCAAGATGTTCCCTGTCCTGGAGG 183
DB 241 CCGTGGTGTACTCAGCTCAGACTCTGATACCTACCAAGATGTTCCCTGTCCTGGAGG 300
QY 184 TAGTAATGCTGGGCAATGTACTTCTTCAAGGACAGCAGATTTGCCAGGCAAG 243
DB 301 TAGTAATGCTGGGCAATGTACTTCTTCAAGGACAGCAGATTTGCCAGGCAAG 360
QY 244 GGACCTTTGCAATAGACTGGAGCCAGCAATGTCTGAGACGGATCTTGTGCATC 303
DB 361 GGACCTTTGCAATAGACTGGAGCCAGCAATGTCTGAGACGGATCTTGTGCATC 420
QY 304 TGACGCTCTGCTTCTTCAGTGCCTTGTCTGATGTTTCCATGATACAGATGAT 363
DB 421 TGACGCTCTGCTTCTTCAGTGCCTTGTCTGATGTTTCCATGATACAGATGAT 480
QY 364 GAGGCAAGGCTCATTTTCTGTTTGTCTTCTTGGGATCTGGGATCCACACGCTAGC 423
DB 481 GAGGCAAGGCTCATTTTCTGTTTGTCTTCTTGGGATCTGGGATCCACACGCTAGC 540
QY 424 CATCTNCACTTCTACTTTGGGAAACCCAGCGCGGAAAGCCAAAGGCTTATGAGCCACACA 483
DB 541 CATCTNCACTTCTACTTTGGGAAACCCAGCGCGGAAAGCCAAAGGCTTATGAGCCACACA 600

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

484 AGACTT 489
501 AGACTT 606

RESULT 4
AA017836/c
LOCUS
DEFINITION
AA017836
ACCSSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

512 bp mRNA linear EST 21-JAN-1997
mb4403.r1 Soares mouse placenta 4NDMP13.5 14.5 Mus musculus cDNA
Clone IMAGE:445397 5', mRNA sequence.
AA017836
AA017836.1 GI:1481103
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 512)
Marra, M., Hillier, D., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousees@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:270733
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 466.
Location/Qualifiers
1..512
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/dev_stage="adult"
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/clone_lib="Soares mouse placenta 4NDMP13.5 14.5"
/note="Organ: placenta; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTACCAATCTCAAGTGGAGCGCGGAAATTTTTTTTTTTTTTTTTTTTTT
T 3']"; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 96.4%; Score 471.4; DB 9; Length 512;
Best Local Similarity 99.2%; Pred. No. 3.5e-131;
Matches 483; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 4 TGAGGCTAGATCTTCAGAACTGTTCCTG-AGGATCCTGTGTCACAACTTTTACAGGCTT 62
DB 506 TGGGGCTAGATCTTCAGAACTGTTCCTGAGGATCCTGTGTCACAACTTTTACAGGCTT 447
QY 63 ATACTGCTATTATCATAGACTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACCT 122
DB 446 ATACTGCTATTATCATAGACTTCAGGCAAACTCTCTCAAGGATGATTTGGCCAAACCT 387

QY 123 TCCGTGGGTTTACTCAGCTCAGACTCTGATCTACCAAGATGTTCCCTGCTCTGGAG 182
 Db 386 TCCGTGGGTTTACTCAGCTCAGACTCTGATCTACCAAGATGTTCCCTGCTCTGGAG 327
 QY 183 GTAGTAATGCTGGGCAATGTTACTTCTTTCAAGGACAAGAGATTTGCCAAGGGCAAA 242
 Db 326 GTAGTAATGCTGGGCAATGTTACTTCTTTCAAGGACAAGAGATTTGCCAAGGGCAAA 267
 QY 243 GGGACCTTTTGCATATAGACTGGAAGCCAGAAATGCTCTGAGACGAGATCTTGTGCAT 302
 Db 266 GGGACCTTTTGCATATAGACTGGAAGCCAGAAATGCTCTGAGACGAGATCTTGTGCAT 207
 QY 303 CTGACGCTCTGCTGCTTTTTCAGTGCCTTTGCTGATGCTTTCCATGGATACAAGTGTA 362
 Db 206 CTGACGCTCTGCTGCTTTTTCAGTGCCTTTGCTGATGCTTTCCATGGATACAAGTGTA 147
 QY 363 TGAGGCAAGGCTCAATTTTCACTGCTTATGTTCTTTTGGGATCTGGGATCCACACGCTAG 422
 Db 146 TGAGGCAAGGCTCAATTTTCACTGCTTATGTTCTTTTGGGATCTGGGATCCACACGCTAG 87
 QY 423 CCATCTTCATTTCTACTTTTGGGCAACCCAGCGCCGGAAGCAAGGCTTTCATGAGCCACAC 482
 Db 86 CCATCTTCATTTCTACTTTTGGGCAACCCAGCGCCGGAAGCAAGGCTTTCATGAGCCACAC 27
 QY 483 AAGACTT 489
 Db 26 AAGACTT 20

RESULT 5
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 LOCUS
 DEFINITION UI-M-GL0-cfw-n-02-0-UI.r1 NIH BMAP_GLO Mus musculus cDNA clone
 IMAGE:30358681 5', mRNA sequence.
 CD364102
 CD364102.1 GI:31144939

EST.
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
 http://genome.uiowa.edu/distribution/mousefl.html
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

The following repetitive elements were found in this cDNA
 sequence: 258-287, >RUTR5_MM4LTR/Retroviral (matched complement)
 Seq primer: PYX-5.
 FEATURES
 Location/Qualifiers
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 /mol_type="mRNA"
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 /dev_stage="1, 5 and 15 days newborn"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH_BMAP_GLO"
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I;
 Site 2: Not I; The library was constructed according
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
 1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT
 primer containing a Not I site. Double strand cDNA was size
 selected according to mRNA size fraction, ligated with
 Ecor I adaptor, digested with NotI and then cloned
 directionally into pYX-Asc vector. The library tag
 sequence located between the Not I site and the polyA tail
 is CCAACTGAAT. This library was created for the University
 of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
 Developing Mouse Nervous System', supported by National
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
 program coordinator."

ORIGIN

Query Match 96.4%; Score 471.4; DB 14; Length 762;
 Best Local Similarity 99.2%; Pred. No. 4.3e-131;
 Matches 483; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 4 TGAGGCTAGATCTTCAAGAACTGTTCCCTG-AGGATCTGTCCTCAAGCTTTTTCAGGCTT 62
 Db 225 TGGGCTAGATCTTCAAGAACTGTTCCCTGAAGGATCTGTCCTCAAGCTTTTTCAGGCTT 284
 QY 63 ATACTGCTATTATCATAGACCTTCAGGCAAAATCTCTCAAGGATGATTTGCGCAACCT 122
 Db 295 ATACTGCTATTATCATAGACCTTCAGGCAAAATCTCTCAAGGATGATTTGCGCAACCT 344
 QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGATGTTCCCTGCTCTGGAG 182
 Db 345 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGATGTTCCCTGCTCTGGAG 404
 QY 183 GTAGTAATGCTGGGCAATGTTACTTCTTTCAAGGACAAGCAGATTTGCCAAGGGCAAA 242
 Db 405 GTAGTAATGCTGGGCAATGTTACTTCTTTCAAGGACAAGCAGATTTGCCAAGGGCAAA 464
 QY 243 GGGACCTTTTGCATATAGACTGGAAGCCAGAAATGCTCTGAGACGAGATCTTGTGCAT 302
 Db 465 GGGACCTTTTGCATATAGACTGGAAGCCAGAAATGCTCTGAGACGAGATCTTGTGCAT 524
 QY 303 CTGACGCTCTGCTGCTTTTTCAGTGCCTTTGCTGATGCTTTCCATGGATACAAGTGTA 362
 Db 525 CTGACGCTCTGCTGCTTTTTCAGTGCCTTTGCTGATGCTTTCCATGGATACAAGTGTA 584
 QY 363 TGAGGCAAGGCTCAATTTTCACTGCTTATGTTCTTTGGGATCTGGGATCCACACGCTAG 422
 Db 585 TGAGGCAAGGCTCAATTTTCACTGCTTATGTTCTTTGGGATCTGGGATCCACACGCTAG 644
 QY 423 CCATCTTCATTTCTACTTTTGGGCAACCCAGCGCCGGAAGCAAGGCTTTCATGAGCCACAC 482
 Db 645 CCATCTTCATTTCTACTTTTGGGCAACCCAGCGCCGGAAGCAAGGCTTTCATGAGCCACAC 704
 QY 483 AAGACTT 489
 Db 705 AAGACTT 711

RESULT 6
 AU080019
 LOCUS
 DEFINITION Sugano mouse brain mncb Mus musculus cDNA clone MNCb-5090
 5', mRNA sequence.
 AU080019
 AU080019.1 GI:6084774

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 791)
 Hashimoto, K., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Toyoda, A.,
 Suzuki, Y., Sasaki, M., and Sugano, S.
 Isolation of full-length cDNA clones from a mouse brain cDNA
 library made by oligo-capping method
 Unpublished (1999)
 Contact: Katsuyuki Hashimoto

Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.

FEATURES

source
1..791
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="MNCB-5090"
/sex="female"
/dev_stages="adult"
/lab_host="TOP10"
/clone_lib="Sugano mouse brain mncb"
/note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA was primed with an oligo(dT) primer
ATGTGGCTTTTCTTTTCTTTT; double-stranded cDNA was ligated into a DralII adaptor (TGTGGCTACTGG), digested and sites just outside the DralII sites can be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5 kb. Library was constructed by Sugano et al. (University of Tokyo, Institute of Medical Science).
Custom primer used for sequencing: 5' end primer [CTTCTGCTTAAAGCTGG], 3' end primer [CGACCTGACCTGAGCACA]"

ORIGIN

Query Match 96.4%; Score 471.4; DB 9; Length 791;
Best Local Similarity 99.4%; Pred. No. 4.4e-131;
Matches 484; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 4 TGAGGCTAGATCTTCAGAACTGTCCTG-AGGATCTGGTCCAAACTTTTACAGGCTT 62
DB 202 TGGGGCTAGATCTTCAGAACTGTCCTGAGGATCTGGTCCAAACTTTTACAGGCTT 261
QY 63 ATACTGCTATTATCATAGACCTTCAGGAAATCTCTCAAGATGATTTGGCCACACCT 122
DB 262 ATACTGCTATTATCATAGACCTTCAGGAAATCTCTCAAGATGATTTGGCCACACCT 321
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTCCTGTCTGGAG 182
DB 322 TCCGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTCCTGTCTGGAG 381
QY 183 GTAGTAATGCTCGGACATGTTACTCTTTCAAGACACAGCAGATTTGCCAAGGCAA 242
DB 382 GTAGTAATGCTCGGACATGTTACTCTTTCAAGACACAGCAGATTTGCCAAGGCAA 441
QY 243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCTCAGAACGATCTTTGTGCAT 302
DB 442 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCTCAGAACGATCTTTGTGCAT 501
QY 303 CTGACGGTCTGGTCTTTTGCAGTGGGTTTGTGCTGATGGTTTCCATGGATACAAAGTGA 362
DB 502 CTGACGGTCTGGTCTTTTGCAGTGGGTTTGTGCTGATGGTTTCCATGGATACAAAGTGA 561
QY 363 TGAGGACAGGCTCATTTTTCACGCTTATGTTCTTTTGGGATCTGGGATCCACCGCTAG 422
DB 562 TGAGGACAGGCTCATTTTTCACGCTTATGTTCTTTTGGGATCTGGGATCCACCGCTAG 621
QY 423 CCATCTNCATTTACTTTGGGAAACCCAGCGCCGAAAGCCAGGCTTTATGAGCCAC 482
DB 622 CCATCTNCATTTACTTTGGGAAACCCAGCGCCGAAAGCCAGGCTTTATGAGCCAC 681
QY 483 AAGACTT 489
DB 682 AAGACTT 688

RESULT 7
CK128347

LOCUS CK128347 838 bp mRNA linear EST 02-DEC-2003
DEFINITION AGENCOURT_16686175 NIH MGC_203 Mus musculus cDNA clone
IMAGE:30790255 5', mRNA sequence.
ACCESSION CK128347
VERSION CK128347.1 GI:38618771
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 838)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: gqabbs@mail.nih.gov
Tissue Procurement: Naryan Bhat
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAMI07 row: d column: 08
High quality sequence stop: 717.

FEATURES

source
1..838
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30790255"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 203"
/note="Organ: placenta; Vector: pExpress-1; Site: 1; EcorV; female C57/BL6 mouse at 16 days pregnancy. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (TRI-reagent method). cDNA was primed using oligo-dT primer:
5'-pGACTGATCTAGTCGAGCGCGCCGCTT25-3' and cloned into the EcorV/NotI sites of pExpress-1. Size-selection >1kb resulted in an average insert size of 1.3 kb. This primary, microquantity library is normalized to Cot5 (non-normalized primary library is NIH MGC 222) and was constructed by Express Genomics (Frederick, MD)."

ORIGIN

Query Match 96.4%; Score 471.4; DB 14; Length 838;
Best Local Similarity 99.2%; Pred. No. 4.5e-131;
Matches 483; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 4 TGAGGCTAGATCTTCAGAACTGTCCTG-AGGATCTGGTCCAAACTTTTACAGGCTT 62
DB 120 TGGGGCTAGATCTTCAGAACTGTCCTGAGGATCTGGTCCAAACTTTTACAGGCTT 179
QY 63 ATACTGCTATTATCATAGACCTTCAGGAAATCTCTCAAGATGATTTGGCCACACCT 122
DB 180 ATACTGCTATTATCATAGACCTTCAGGAAATCTCTCAAGATGATTTGGCCACACCT 239
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGTCTGGAG 182
DB 240 TCCGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGTCTGGAG 299
QY 183 GTAGTAATGCTCGGACATGTTACTCTTTTCAAGACACAGCAGATTTGCCAAGGCAA 242
DB 300 GTAGTAATGCTCGGACATGTTACTCTTTTCAAGACACAGCAGATTTGCCAAGGCAA 359
QY 243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCTCTGAGAACGATCTTTGTGCAT 302
DB 360 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCTCTGAGAACGATCTTTGTGCAT 419

QY 303 CTGACGGTCTGCTCTTTTCAGTGGCTTTGCTGATGGTTTCCATGATCAAGTGTA 362
 Db 420 CTGACGGTCTGCTCTTTTCAGTGGCTTTGCTGATGGTTTCCATGATCAAGTGTA 479
 QY 363 TGAGGAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATTTGGGATCCACACGCTAG 422
 Db 480 TGAGGAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATTTGGGATCCACACGCTAG 539
 QY 423 CCATCTNCATTTCTTTTGGGAGACCGAGCGCGGAAAGCCAAAGGCTTATGAGCCACAC 482
 Db 540 CCATCTNCATTTCTTTTGGGAGACCGAGCGCGGAAAGCCAAAGGCTTATGAGCCACAC 599
 QY 483 AAGACTT 489
 Db 600 AAGACTT 606
 RESULT 8
 LOCUS BC038338/c 884 bp mRNA linear HTC 01-OCT-2002
 DEFINITION Mus musculus, clone IMAGE:1513950, mRNA.
 ACCESSION BC038338
 VERSION BC038338.1 GI:23398571
 KEYWORDS HTC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 884)
 Strausberg, R.
 Direct Submission
 Submitted (01-OCT-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: Marcello Bento Soares, Ph.D.
 cDNA Library Preparation: Soares Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: amadansystemsbiology.org
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 83 Row: k Column: 11
 This clone has the following problem: no polyA-tail.
 Location/Qualifiers
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 /db_xref="taxon:10090"
 /clone="IMAGE:1513950"
 /tissue_type="Mammary gland, lactating mouse"
 /clone_lib="Soares_mammary_gland_NMLMG"
 /lab_host="DH103"
 /note="Vector: p773D-Pac"
 ORIGIN
 Query Match 96.4%; Score 471.4; DB 11; Length 884;
 Best Local Similarity 99.2%; Pred. No. 4.7e-131;
 Matches 483; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
 QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCTG-AGGATCCTGTCAGAACTTTTACAGGCTT 62
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 QY 63 ATACTGCTATATCATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCACACCT 122

663 ATACTGCTATATCATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCACACCT 604
 QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATATACACAAAGATGTTCCCTGCTCTGGAG 182
 Db 603 TCCGTGGGTTTACTCAGCTGCAGACTCTGATATACACAAAGATGTTCCCTGCTCTGGAG 544
 QY 183 GTAGTAATGCTGCGGACAAATGTTACTTCTTTCAAGGACAGCAGATTTGCAAGGGGCAA 242
 Db 543 GTAGTAATGCTGCGGACAAATGTTACTTCTTTCAAGGACAGCAGATTTGCAAGGGGCAA 484
 QY 243 GGGACCTTTGCAATAGACACTGGAAAGCCAGAAATGTTCTCTGAGAAACGATTTGTGTCAT 302
 Db 483 GGGACCTTTGCAATAGACACTGGAAAGCCAGAAATGTTCTCTGAGAAACGATTTGTGTCAT 424
 QY 303 CTGACGGTCTGCTGCTTTTTCAGTGGCTTTGCTGATGGTTTCCATGATCAAGTGTA 362
 Db 423 CTGACGGTCTGCTGCTTTTTCAGTGGCTTTGCTGATGGTTTCCATGATCAAGTGTA 364
 QY 363 TGAGGAGGGGCTCATTTTCACTGCTTATGTTCTTTGGGATTTCTGGATCCACACGCTAG 422
 Db 363 TGAGGAGGGGCTCATTTTCACTGCTTATGTTCTTTGGGATTTCTGGATCCACACGCTAG 304
 QY 423 CCATCTNCATTTCTACTTTGGGAAACCGAGCGCGGAAAGCCAAAGGCTTATGAGCCACAC 482
 Db 303 CCATCTNCATTTCTACTTTGGGAAACCGAGCGCGGAAAGCCAAAGGCTTATGAGCCACAC 244
 QY 483 AAGACTT 489
 Db 243 AAGACTT 237
 AK002276 933 bp mRNA linear HTC 20-SEP-2003
 Mus musculus adult male kidney cDNA, RIKEN full-length enriched
 library, clone:0610007C21 product:similar to APOPTOSIS RELATED
 PROTEIN APR-3 (Homo sapiens), full insert sequence.
 AK002276
 AK002276.1 GI:12832140
 HTG; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349836
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
 Iyoda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 4
 RESULT 9
 LOCUS AK002276
 DEFINITION
 ACCESSION AK002276
 VERSION AK002276.1
 KEYWORDS HTG; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349836
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
 Iyoda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 4
 RESULT 9
 LOCUS AK002276
 DEFINITION
 ACCESSION AK002276
 VERSION AK002276.1
 KEYWORDS HTG; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 10349836
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagasaka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
 Iyoda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861
 4

243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCCTGAGAACGGATCTTTGTGCAT 302
Db GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCCTGAGAACGGATCTTTGTGCAT 445
Qy CTGACGGTCTGCTGCTTTGTCAGTGGCTTTGTCGATGGTTCATCGATGATCAAGTGTA 362
Db CTGACGGTCTGCTGCTTTGTCAGTGGCTTTGTCGATGGTTCATCGATGATCAAGTGTA 385
Qy TGAGGACGGCTCAATTTTCACTGCTATGCTTTTGGGATCTTGGGATCCACCGCTAG 422
Db TGAGGACGGCTCAATTTTCACTGCTATGCTTTTGGGATCTTGGGATCCACCGCTAG 325
Qy CCATCTNCAATTTCTATTTGGGAAACCCAGCGCGGAAAGCCAGGCTTATGAGCCACAC 482
Db CCATCTCCATTTCTATTTGGGAAACCCAGCGCGGAAAGCCAGGCTTATGAGCCACAC 265
Qy 483 AAGACTT 489
Db 264 AAGACTT 258

RESULT 12
BE994240
LOCUS
DEFINITION
UI-M-CG0P-bil-g-11-0-UI.s1 NIH_BMAP_Ret4_S2 Mus musculus cDNA clone
UI-M-CG0P-bil-g-11-0-UI 3', mRNA sequence.
ACCESSION
BE994240
VERSION
BE994240.1 GI:10677279
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
COMMENT
97044477
8889548
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
Oligo-dt track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
The tissue for this library was contributed by Dr. Xin-Yuan Fu,
Yale University School of Medicine The following repetitive
elements were found in this cDNA sequence: 202-231,
>RLTR5_MM#LTR/Retroviral
Seq primer: M3 Forward
POLYA=No.

FEATURES
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1. .669
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/lab_host="DHIOB (Life Technologies)"
/clone_lib="NIH BMAP Ret4 S2"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker: Site 1: Not I; Site 2: Eco RI; The
NIH BMAP_Ret4_S2 library is a subtracted library,
ultimately derived from mouse retina tissue libraries at

various stages of development. For a detailed description
of the library from which this clone was derived, please
visit our web site at brainest.eng.uiowa.edu. The tissue
for this library was contributed by Dr. Xin-Yuan Fu, Yale
University School of Medicine
TAG_SEQ=None found"

ORIGIN
Query Match 93.3%; Score 456.2; DB 10; Length 669;
Best Local Similarity 98.6%; Pred. No. 1.6e-126;
Matches 480; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

Qy 4 TGAGGCTAGATCTTCAGAACTGTTCCCTG-AGGATCTCGTCCAAACTTTTTCAGAGCTT 62
Db 169 TGGGGCTAGATCTTCAGAACTGTTCCCTGAAAGATCTCGTCCAAACTTTTTCAGAGCTT 228
Qy 63 ATACTGCTATTATCATAGACCTTCAGCAATCTCTCAAGGATGATTTGGCCAAACACCT 122
Db 229 ATACTGCTATTATCATAGACCTTCAGCAATCTCTCAAGGATGATTTGGCCAAACACCT 288
Qy 123 TCGTGGTATTACTCAGCTCAGACTCTGATATACCAAGATGTTCCCTGCTCGGAG 182
Db 289 TCGTGGTATTACTCAGCTCAGACTCTGATATACCAAGATGTTCCCTGCTCGGAG 348
Qy 183 GTAGTANTGCTGGGCAATGTTACTTCTTCAAGGACAGCAGATTTGCCAAGGCAAA 242
Db 349 GTAGTANTGCTGGGCAATGTTACTTCTTCAAGGACAGCAGATTTGCCAAGGCAAA 408
Qy 243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCCTGAGAACGGATCTTTGTGCAT 302
Db 409 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCCTGAGAACGGATCTTTGTGCAT 468
Qy 303 CTGACGGTCTGCTCTTTTCAGTGGCTTTGTCGATGATGTTTCCATGATGATCAAGTGTA 362
Db 469 CTGACGGTCTGCTCTTTTCAGTGGCTTTGTCGATGATGTTTCCATGATGATCAAGTGTA 528
Qy 363 TGAGGACGGCTCATTTTCACTGCTATGTTCTTTGGGATCTTGGGATCCACCAACCGTAG 422
Db 529 TGAGGACGGCTCATTTTCACTGCTATGTTCTTTGGGATCTTGGGATCCACCAACCGTAG 588
Qy 423 CCATCTNCAATTTCTATTTGGGAAACCCAGCGCGGAAAGCCAGGCTTATGAGCCACAC 482
Db 589 CCATCTCCATTTCTATTTGGGAAACCCAGCGCGGAAAGCC-AGGTTCTATGAGCCACAC 647
Qy 483 AAGACTT 489
Db 648 AAGACTT 654

RESULT 13
CGS89400
LOCUS
DEFINITION
CGS89400 Mus musculus 1298v/Ev Mus musculus genomic clone
CGS89400, genomic survey sequence.
ACCESSION
CGS89400
VERSION
CGS89400.1 GI:37395179
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 635)
Zambrowicz,B.P., Abuin,A., Ramirez-Solis,R., Richter,L.J.,
Piggott,J., BeltrandelRio,H., Buxton,E.C., Edwards,J., Finch,R.A.,
Fridde,C.J., Gupta,A., Hansen,G., Hu,Y., Huang,W., Jaing,C.,
Key,B.W. Jr., Kipp,P., Kohlhauff,B., Ma,Z.-Q., Markesich,D.,
Payne,R., Potter,D.G., Qian,N., Shaw,J., Schrick,J., Shi,Z.-Z.,
Sparks,M.J., Van Sligtenhorst,I., Vogel,P., Walke,W., Xu,N.,
Zhu,Q., Person,C. and Sands,A.T.
Wnk1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP

```

OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.

FEATURES             Location/Qualifiers
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Query Match          91.9%; Score 449.2; DB 29; Length 635;
Best Local Similarity 97.1%; Pred. No. 2e-124;
Matches 473; Conservative 0; Mismatches 12; Indels 2; Gaps 2;

Qy 4 TGAGGCTAGATCTTCAGAACTGTTCCTG-AGGATCTGTGTCACAACTTTTACAGGCTT 62
Db 115 TGGGGCTAGATCTTCAGAACTGTTCCTGAGGATCTGNCACAACTTTTACAGGCTT 174

Qy 63 ATACTGCTATTATCATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCACACCT 122
Db 175 ATACTGCTATTATCATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCACANNCT 234

Qy 123 TCGGTGGTTTACTACGCTGACACTCTGATACCTACACAAAGATGTTCCCTGTCCTGGAG 182
Db 235 TCGGTGGTTTACTCAGNTGCAGACTCTGATACCTACACAAAGATGTTCCCTGTCCTGGAG 294

Qy 183 GTAGTAATGCTGGGCAATGTACTTCTTCAAGGACAGAGATTTGCCAAGGGCAAA 242
Db 295 GTANTATGCTGGGCAATGTACTTCTTCAAGGACAGAGATTTGCCAAGGGCAAA 354

Qy 243 GGGACCTTTGCAATAGCACTGGAAGCCAGCAATGTCTCTGAGAACGGATCTTGTCAT 302
Db 355 GGGACCTTTGCAATAGCACTGGAAGCCAGCAATGTCTCTGAGAACGGATCTTGTCAT 414

Qy 303 CTGACGCTCTGCTCTTTCAGTGGGTTTGCTGATGTTTCCATGGATACCAAGTGA 362
Db 415 CTGACGCTCTGCTCTTTCAGTGGGTTTGCTGATGTTTCCATGGATACCAAGTGA 474

Qy 363 TGAGGCAAGGCTCATTTTCACTGTTATGTTCTTGGGATCTGGGATCCACACGCTAG 422
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Qy 423 CCATCTNCATCTACITTTGGGACCCAGCGCCGGAAGCCAGAGCTTATGAGCCACAC 482
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Qy 483 AAGACTT 489
Db 594 AAGACTT 600

RESULT 14
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DEFINITION UT-M-FB0-bxy-b-08-0-UI.r1 NIH BMAP_FBO Mus musculus cDNA clone
INSDC       IMAGE:5714559 5', mRNA sequence.
ACCESSION  BQ748981
VERSION    BQ748981.1  GI:21895768
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 720)
AUTHORS    NIH-MGC http://mgc.nci.nih.gov/

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TITLE
JOURNAL
COMMENT
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgspps-remail.nih.gov
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this cDNA
sequence: 239-268, >RLTR5_MM#LTR/Retroviral (matched complement)
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Location/Qualifiers
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/strain="C57BL/6"
/db_xref="taxon:10090"
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/tissue_type="whole brain"
/dev_stage="embryo 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP FBO"
/notes="Organ: brain; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA
tail, is TGAGGACCC. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP). 'Gene Discovery in the Developing Mouse Nervous
System', supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

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ORIGIN
Query Match          91.6%; Score 447.8; DB 13; Length 720;
Best Local Similarity 99.1%; Pred. No. 5.7e-124;
Matches 460; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 4 TGAGGCTAGATCTTCAGAACTGTTCCTG-AGGATCTGTGTCACAACTTTTACAGGCTT 62
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Qy 63 ATACTGCTATTATCATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCACACCT 122
Db 266 ATACTGCTATTATCATAGACCTTCAGGCAAACTCTCTCAAGGATGATTTGGCCACACCT 325

Qy 123 TCCGTGGGTTTACTCAGCTGACACTCTGATACCTACCAAGATGTTCCCTGTCTCTGGAG 182
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Qy 183 GTAGTAATGCTGGGCAAACTTTACTTCTTTCAGGACAAAGAGATTTGCCAAGGGCAAA 242
Db 386 GTAGTAATGCTGGGCAAACTTTACTTCTTTCAGGACAAAGAGATTTGCCAAGGGCAAA 445

Qy 243 GGGACCTTTGCAATAGCACTGGAAGCCAGCAATGTCTCTGAGAACGGATCTTGTCAT 302
Db 446 GGGACCTTTGCAATAGCACTGGAAGCCAGCAATGTCTCTGAGAACGGATCTTGTCAT 505

Qy 303 CTGACGCTCTGCTCTTTCAGTGGGTTTGCTGATGTTTCCATGGATACCAAGTGA 362
Db 506 CTGACGCTCTGCTCTTTCAGTGGGTTTGCTGATGTTTCCATGGATACCAAGTGA 565

Qy 363 TGAGCAGGGCTCATTTTCACTGCTTATGTTCTTGGGATCTGGGATCCACACGCTAG 422

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Db 566 TGAGCAGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGATCCACCGCTAG 625
QY 423 CCATCTNCATCTACTTTGGGGAACCCAGCGCCGGAAGCAAG 466
Db 626 CCATCTCCATCTACTTTGGGGAACCCAGCGCCGGAAGCAAG 669

RESULT 15
BX520494
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BX520494 469 bp mRNA linear EST 27-JUN-2003
BX520494 Sugano mouse kidney mKia Mus musculus cDNA clone
IMAGE:998H105621 ; IMAGE:2270265, mRNA sequence.

BX520494
BX520494.1 GI:32295561
EST.
Mus musculus (house mouse)

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 469)
Heil, O., Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D.
and Korn, B.
Mouse Unigeneset - RZPD2
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE:998H105621.
RZPDLIB, I.M.A.G.E. cDNA Clone Collection;
Mouse Unigeneset - RZPD2 (RZPDLIB No.981)
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=981 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
sugF, Primer sequence: CTCTGCTCTAAAGCTGGC.

FEATURES
Location/Qualifiers
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/sex="female"
/dev_stage="adult"
/lab_host="DH108"
/clone_lib="Sugano mouse kidney mKia"
/notes="Organ: kidney; Vector: pME18S-FL3; Site 1: DralII
(CACTGTGTG); Site 2: DralII (CACCAATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was
ligated to a DralII adaptor [TGTGGCTACTGTG], digested
and cloned into distinct DralII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCAATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTCTGCTCTAAAGCTGGC and 3' end
primer CGACCTGCAGCTCGAGACA."

ORIGIN
Query Match 91.3%; Score 446.4; DB 13; Length 469;
Best Local Similarity 99.3%; Pred. No. 1.2e-123;
Matches 447; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 40 TGGTCCAACTTTTACAGGCTTATAGCTATATCATAGACCTTCAGGCAAACTCTCT 99

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QY 100 CAAGGATGATTTCGGCAACACCTTCCTGGGTTTACTCAGCTGCAGACTCTGATACTACC 159
Db 61 CAAGGATGATTTCGGCAACACCTTCCTGGGTTTACTCAGCTGCAGACTCTGATACTACC 120
QY 160 ACAAGATGTTTCCTGCTCCTGGAGGTAGTATGCTGGGACAATGTTACTTCTTTCAAGGA 219
Db 121 ACAAGATGTTTCCTGCTCCTGGAGGTAGTATGCTGGGACAATGTTACTTCTTTCAAGGA 180
QY 220 CAAGCAGATTTCGCAAGGCAAGGGACCTTTTCAATAGCAGCTGGAAGCCAGAAATGTG 279
Db 181 CAAGCAGATTTCGCAAGGCAAGGGACCTTTTCAATAGCAGCTGGAAGCCAGAAATGTG 240
QY 280 TCCTGAGAACGGATCTTTGTGCATCTGACGCTCCTGCTTTTTCAGTGCCTTTTGTGCTGA 339
Db 241 TCCTGAGAACGGATCTTTGTGCATCTGACGCTCCTGCTTTTTCAGTGCCTTTTGTGCTGA 300
QY 340 TGGTTTCATCGGATACAGTGTATGAGGCAAGGCTCATTTTCACTGCTTATGTTCTTTGG 399
Db 301 TGGTTTCATCGGATACAGTGTATGAGGCAAGGCTCATTTTCACTGCTTATGTTCTTTGG 360
QY 400 GATTCTGGGATCCACACGCTAGCCATCTTCAATTTTGGGGAACCCAGGCGCGGAA 459
Db 361 GATTCTGGGATCCACACGCTAGCCATCTTCAATTTTGGGGAACCCAGGCGCGGAA 420
QY 460 AGCCAAAGCTTTATGAGCCACACAAAGCTT 489
Db 421 AGCCAAAGCTTTATGAGCCACACAAAGCTT 450

Search completed: June 25, 2004, 23:31:15
Job time : 2001 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 20:27:06 ; Search time 64 Seconds
(without alignments)
4240.172 Million cell updates/sec

Title: US-09-773-476-294
Perfect score: 489
Sequence: 1 gactgaggttagattcttag.....tnatgagccacacaagactt 489

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 582709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/prodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	182.6	37.3	524	4	US-09-621-976-1403 Sequence 1403, Ap
2	165	33.7	498	4	US-09-621-976-2829 Sequence 2829, Ap
3	45.4	9.3	452	4	US-09-621-976-16474 Sequence 16474, A
4	34.4	7.0	474	4	US-09-621-976-18033 Sequence 18033, A
5	31.8	6.5	2196	4	US-09-540-236-124 Sequence 124, App
6	31.8	6.5	65792	4	US-09-596-002-31 Sequence 31, Appl
7	30.8	6.3	1515	4	US-09-134-000C-2080 Sequence 2080, Ap
8	30.4	6.2	1089	4	US-09-543-681A-895 Sequence 895, App
9	30.4	6.2	1725	4	US-09-543-681A-2148 Sequence 2148, Ap
10	30	6.1	374	3	US-08-638-931-48 Sequence 48, Appl
11	29.8	6.1	2859	4	US-09-328-352-425 Sequence 425, App
12	29.6	6.1	851	4	US-09-598-401C-22 Sequence 22, Appl
13	29.4	6.0	894	3	US-09-328-111-616 Sequence 616, App
14	29.4	6.0	832	4	US-09-621-976-2813 Sequence 2813, Ap
15	29.4	6.0	7100	4	US-09-308-375-1 Sequence 1, Appl
16	29.4	6.0	7766	4	US-09-125-619-3 Sequence 3, Appl
17	29	5.9	442	4	US-09-227-357-132 Sequence 132, App
18	29	5.9	5837	1	US-07-686-340-1 Sequence 1, Appl
19	29	5.9	5837	1	US-08-004-139B-1 Sequence 1, Appl
20	29	5.9	5837	1	US-08-117-491-1 Sequence 1, Appl
21	29	5.9	5837	1	US-08-271-364A-1 Sequence 1, Appl
22	29	5.9	5837	2	US-08-811-492-1 Sequence 1, Appl
23	29	5.9	5837	2	US-08-222-715B-1 Sequence 1, Appl
24	29	5.9	5837	5	PCT-US96-1054A-1 Sequence 1, Appl
25	29	5.9	5837	4	US-09-803-671B-3 Sequence 3, Appl
26	28.8	5.9	359	4	US-08-838-931-51 Sequence 51, Appl
27	28.6	5.8	3504	2	US-08-760-797A-2 Sequence 2, Appl

C 28	28.6	5.8	3504	2	US-08-760-797A-4	Sequence 4, Appl
C 29	28.6	5.8	3504	3	US-08-932-929B-2	Sequence 2, Appl
C 30	28.6	5.8	3504	3	US-08-932-929B-4	Sequence 4, Appl
C 31	28.4	5.8	1353	4	US-08-956-171B-521	Sequence 521, App
C 32	28.4	5.8	1695	4	US-09-142-623-12	Sequence 12, Appl
C 33	28.4	5.8	1809	4	US-09-508-264A-2	Sequence 2, Appl
C 34	28.4	5.8	1859	4	US-09-508-264A-7	Sequence 7, Appl
C 35	28.4	5.8	2560	5	PCT-US92-05707-1	Sequence 1, Appl
C 36	28.2	5.8	750	4	US-09-134-001C-514	Sequence 514, App
C 37	28.2	5.8	786	1	US-08-345-756-1	Sequence 1, Appl
C 38	28.2	5.8	786	1	US-08-625-198-1	Sequence 1, Appl
C 39	28.2	5.8	886	6	5219739-23	Patent No. 5219739
C 40	28.2	5.8	2039	1	US-08-345-756-5	Sequence 5, Appl
C 41	28.2	5.8	2039	1	US-08-625-198-5	Sequence 5, Appl
C 42	28.2	5.8	24183	3	US-08-943-731-3	Sequence 3, Appl
C 43	28	5.7	466	4	US-09-833-381-842	Sequence 842, App
C 44	28	5.7	2119	4	US-09-240-639-7	Sequence 7, Appl
C 45	28	5.7	5506	4	US-09-976-594-530	Sequence 530, App

ALIGNMENTS

RESULT 1

US-09-621-976-1403
; Sequence 1403, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1403
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..504
; NAME/KEY: sig_peptide
; LOCATION: 10..99
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 8.80000019073486
; OTHER INFORMATION: seq ALLLALGVERALA/LP
US-09-621-976-1403

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Matches 245;	Conservative 1;				
QY	4	TCAGGCTAGATCTTCAGAACTGTTCCTT-GAGGATCTCTGGTCCAACTTTTACAGGCTT	62		
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QY	63	ATAGTCTTATCATATAGACCTTCAGCAATCTCTCAAGATGATTGGCCACACCT	122		
Db	287	ATACCACCTGTCATCATAGACCTGCAAGCAACCCCTCAAAGGTGACTTGGCCACACCT	346		
QY	123	TCCGTGGTGTTCAGTCTGAGACTCTGATCTACCAAGATGTTCCTGTCTGGAG	182		
Db	347	TCCGTGGTGTTCAGTCTGAGACTCTGATCTGACCAACATGTCACTGTCTGGAG	406		
QY	183	GTAGTAATGCTGGACAATTTACTTTTCAAGGACAAGATTGGCAAGGCAAA	242		
Db	407	GAATTAATGCTGGAACTACTATCCTCTTATATAGACACCAAACTGTCAA-GGCAAA	465		
QY	243	GGGACCTTTGCAATAGACTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTTGTGCA	301		

Db 466 AGRACCTTTGCAATAACACTGG-GGACCAGAAATGTGTCTGAGATGGATCTTGTGTA 523

RESULT 2

US-09-621-976-2829
; Sequence 2829, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2829
; LENGTH: 498
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 155..391
US-09-621-976-2829

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Best Local Similarity 87.2%; Pred. No. 4.6e-49;
Matches 191; Conservative 0; Mismatches 27; Indels 1; Gaps 1;
QY 272 GAATGTGTCTGAGACGATCTTGGCATCTGACGGTCTGTGCTTTTGGAGTGGT 331
Db 152 GAATGTGTCTGAGATGGATCTTGTACCTGATGCTCCAGGCTTTTGCAGTGT 211
QY 332 TGTCTGATGTTTCCATGGATCAAGTGTAT-CAGGACGGCTCATTTTCACTGCTTAT 390
Db 212 TGTCTGATGTTTCCATGGATCAAGTGTATGCGCCAGGCTCTTCTCATGCTTAT 271
QY 391 GTTCTTTGGGATTCGGATCCACACGCTAGCATCTNCACTTACTTTGGGAACCCA 450
Db 272 GTTCTTGGGATTCGGAGCCACCACTATCGCTTCCATCTGCTTTGGGCGACCCA 331
QY 451 GCGCCGAAAGCCCAAGCTTATGAGCCACACAGACTT 489
Db 332 GCGCCGAAAGCCCAAGCTTATGAGCTTATGAGCTT 370

RESULT 3

US-09-621-976-16474
; Sequence 16474, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 16474
; LENGTH: 452
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-16474

Query Match 9.3%; Score 45.4; DB 4; Length 452;
Best Local Similarity 73.4%; Pred. No. 4.2e-06;
Matches 58; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCTGAGGATCCTGTCCTGCTTTCAGGCTTA 63

Db 374 TGGGGTGGATCTCCAGAACTGTTCTCTGGAGGACCCCTGGTCAAACCTTTCATCAGGCACA 433
QY 64 TACTGCTATTATCATAGAC 82
Db 434 TACCACTGTCATCATAGAC 452

RESULT 4

US-09-621-976-18033
; Sequence 18033, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18033
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 16
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-18033

Query Match 7.0%; Score 34.4; DB 4; Length 474;
Best Local Similarity 16.9%; Pred. No. 0.039;
Matches 53; Conservative 115; Mismatches 146; Indels 0; Gaps 0;
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QY 109 TTTGCCAACCTTCCGTGGTTTACTCAGCTCAGACTCTGATCTACCAAGATGT 168
Db 212 MSKTWCCMACCMCMCRRARSCMRSCNRSYTYMVCYMYMYKGGMYWWRGSMWR 271
QY 169 TCCCTGTCTCGAGGTAGTAACTGCTGGACAATGTTACTTCTTCAAGGACAGCAGAT 228
Db 272 MYMYTKKSMWRGSCMWRKAWARKTYYTWAWYTTTYKEMCCYMKRTTCMMMYSR 331

QY 229 TTGCCAAGGCAAGGGACCTTTGCAATAGCACTGGAGCCAGAAATGTCTCTGAGAA 288
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QY 289 CGGATCTTGTGCACTGACGTCCTGGTCTTTTCGAGTGGCTTTGTGCTGATGTTTCCA 348
Db 392 TGTCTCATGCTCTGTAATCCAGCACTTTGGGATGCMARKYKGRGRGWYCYTTKRGSCM 451
QY 349 TGGATACAAAGTGA 362
Db 452 RGRKTCGAGAGCA 465

RESULT 5

US-09-540-236-124/c
; Sequence 124, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARF
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 124

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; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2080
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2080

Query Match
Best Local Similarity 6.3%; Score 30.8; DB 4; Length 1515;
Matches 62; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 106 TGATTGGCCAAACACCTTCGCTGGGTTTACTAGCTCAGCTCTGTATACCAAGA 165
Db 344 TGATTAGCAACAATTTTTCAGTTTCTCTGATTCAATTCGTTATTTCTCAGCTACT 285
QY 166 TGTTCCTGCTGCTGGAGGTAGTAATGCTGGCAATGTTACTTCTTTCAAGGA 219
Db 284 TGTGCCAAGTAATGAAAGTCGTTCAATCTTTGAACCTTTCTTATCTGATTGA 231

RESULT 8
US-09-543-681A-895
; Sequence 895, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 895
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-895

Query Match
Best Local Similarity 6.2%; Score 30.4; DB 4; Length 1089;
Matches 76; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 132 TTACTAGCTGCAGACTCTGATACTACTACCAAGATGTTCCCTGCTGGAGGTAGTAATG 191
Db 518 TTAATGAATTCCTATATAACCAAGAAAGTTTGTTCATCTAATCCAGAAATTCGATG 577
QY 192 CCTGGCAATGTTACTTCTTCAAGGACAAGCAGATTTGCCAAGGCAAGGACCTTT 251
Db 578 CCGATATAAATTTGGTTTTTACGATGTTTCATATAGTCATGTTCAATAGAAATTTT 637
QY 252 GCAATAGCACTGGAGCCCAAGAAATGTCCT 283
Db 638 CATATACCACAGAGGTTTTCGAACCTATGCT 669

RESULT 9
US-09-543-681A-2148
; Sequence 2148, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
```

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; LENGTH: 2196
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-124

Query Match
Best Local Similarity 6.5%; Score 31.8; DB 4; Length 2196;
Matches 75; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 205 TACTTCTTTCAAGGACAAGCAGATTTCGCAAGGCAAGGACCTTTGCAATAGCACTGG 264
Db 1795 TAATTTCTTTGCTCGCTCAAGATGATAGATAATGGTAAATGCTTGTGCCATGCTGAGT 1736
QY 265 AAGCCAGAAATGTCCTCAGAACGGATCTTGTGATCTGACGTCCTGGTCTTTTGA 324
Db 1735 GTTCGATGACAATGCAAGGATCAGATTGAGCAAAATGGGGTGTGCAATCAGATGCA 1676
QY 325 GTGCGTTTGTGCTGATGGTTTCATGG 351
Db 1675 ATGCGATTTCGGTGATGTCATCGCGG 1649

RESULT 6
US-09-596-002-31
; Sequence 31, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/140,121
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 31
; LENGTH: 65792
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte template ID No. 6632636 31
; PUBLICATION INFORMATION:
US-09-596-002-31

Query Match
Best Local Similarity 6.5%; Score 31.8; DB 4; Length 65792;
Matches 75; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 205 TACTTCTTTCAAGGACAAGCAGATTTCGCAAGGCAAGGACCTTTGCAATAGCACTGG 264
Db 53870 TAATTTCTTTGCTCGCTCAAGATGATTAGATAATGGTAAATGCTTGTGCCATGCTGAGT 53929
QY 265 AAGCCAGAAATGTCCTCAGAACGGATCTTGTGATCTGACGTCCTGGTCTTTTGA 324
Db 53930 GTTCGATGACAATGCAAGGATCAGATTGAGCAAAATGGGGTGTGAATCAGATGCA 53989
QY 325 GTGCGTTTGTGCTGATGGTTTCCATGG 351
Db 53990 ATGCGATTTCGGTGATGTCATCGCGG 54016

RESULT 7
US-09-134-000C-2080/c
; Sequence 2080, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
```

; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 2148
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-2148

Query Match 6.2%; Score 30.4; DB 4; Length 1725;
Best Local Similarity 50.0%; Pred. No. 2.5; Mismatches 0; Indels 0; Gaps 0;
Matches 76; Conservative 0;
QY 132 TTACTAGCTGCAGACTCTGATACACCAAGATGTTCCCTGCTGGAGGTAGTAATG 191
DB 101 TTAATGAATTCCTATATACCAAGCAAGTTTGTTCATCTAATCCAGAATTCGATG 160
QY 192 CTGGGACATGTTACTCTTTCAAGACAAAGCATGTTCCAAAGGCAAGGACCTTT 251
DB 161 CCGATATAAAATTTGGTTTACGATGATTTTCATATTAGTCATGTTCAATAGAATTTT 220
QY 252 GCAATAGCACTGGAAGCCCAAGATGTGCT 283
DB 221 CATATACACAGAGGTTTGCACCTATCT 252

RESULT 10
US-08-638-931-48
; Sequence 48, Application US/08638931
; Patent No. 6194145
; GENERAL INFORMATION:
; APPLICANT: HEIDRICH, Bj rn
; APPLICANT: ROBINSON, Peter-Nicholas
; APPLICANT: TIECKE, Frank
; APPLICANT: ROLFS, Arndt
; TITLE OF INVENTION: Genus and species-specific identification of
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/638,931
; FILING DATE: 25-APR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 195 15 891.1
; FILING DATE: 29-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 374 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:

; ORGANISM: Legionella anisa
; STRAIN: WA-316-C2
; INDIVIDUAL ISOLATE: 24ani
US-08-638-931-48

Query Match 6.1%; Score 30; DB 3; Length 374;
Best Local Similarity 55.9%; Pred. No. 1.3;
Matches 57; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 257 AGCACTGGAAGCCCAAGAAATGTCTGAGAACGGATCTTGTGCATCTGACGGTCTCTGGT 316
DB 63 AGGTGTGAAGCACAGTAATGTGTGAAGCTAACTTGTACTAATTGGCTGATTGCTTGAC 122
QY 317 CTTTTCAGTGCCTTGTGCTGATGGTTTCCATGGATACAAG 358
DB 123 CATATAATCTGAGTTACTTTCAGATTGTGAATGCGAATACAAG 164

RESULT 11
US-09-328-352-425
; Sequence 425, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 425
; LENGTH: 2859
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-425

Query Match 6.1%; Score 29.8; DB 4; Length 2859;
Best Local Similarity 51.1%; Pred. No. 5.8;
Matches 70; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 205 TACTCTTTCAAGACAAAGCATGTTCCAAAGGCAAGGACCTTTGCATACATG 264
DB 744 TAATCATTTGCTCGAACAAAGGTTCCGGAAGGACATATGACCTCACTAAATGAATGA 803
QY 265 AAGCCCAAGAAATGTCTCTGAGAACGGATCTTGTGCATCTGACGGTCTCTTTTGA 324
DB 804 GAGGCTTGAAGCCATCATATATTAGCATTTGCATGAACAGAGGTATCCGACC 863
QY 325 GTGCGTTTGTCTGATG 341
DB 864 GTGGGATTGGGATATTG 880

RESULT 12
US-09-598-401C-22
; Sequence 22, Application US/09598401C
; Patent No. 6596925
; GENERAL INFORMATION:
; APPLICANT: Perera, J. Ranjan
; APPLICANT: Eagleton, Clare
; APPLICANT: Rice, Stephen J.
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1036c2
; CURRENT APPLICATION NUMBER: US/09/598,401C
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 120

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 881
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-598-401C-22

Query Match
  6.1%; Score 29.6; DB 4; Length 881;
Best Local Similarity 56.0%; Pred. No. 3.1;
Matches 56; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 319 TTTCAGTCGCTTGTGCTGATGGTTCCATGATACAAAGTGTATGAGCGAGGCTCAAT 378
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
655 TTTCGCGTGTGTGTGCTGCTGTTTCTTGTGCAAGAGCTATTATGAGGCTCCTTT 714

QY 379 TTCACCTGCTATCTCTTTGGGATCTGGATCCACCAG 418
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
715 GCTCTTCTAGTCTTTTGTCTTCTGTTGTTCCATG 754

RESULT 13
US-09-328-111-616
; Sequence 616, Application US/09328111
; Patent No. 6282333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlesel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 616
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(694)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-616

Query Match
  6.0%; Score 29.4; DB 3; Length 694;
Best Local Similarity 46.9%; Pred. No. 3.1;
Matches 69; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 23 CTGTTCCCTGAGGATCCTGTCACAACTTTTACAGGCTTATCTGCTATTATCATAGAC 82
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
424 CTGACCTTGCRAANCGTGGCATACCTTGGATGTTCCCTTCCATTGGCAAGC 483

QY 83 CTTGAGCAAACTCCTCTCAAGGATGATTTGGCCAAACACCTTCGCTGGGTTTACTAGCTG 142
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
484 CCTTAAACCGGTTTTTCAAGATTTACTGCGNNAACAACTTCNTTCTTTTANGGAATTN 543

QY 143 CAGACTCTGATACACACAGATGTT 169
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
544 GANATNGAANCCCCCAANGAATTT 570
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RESULT 14
US-09-621-976-2813
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.fm
; SEQ ID NO 2813
; LENGTH: 832
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813

Query Match
  6.0%; Score 29.4; DB 4; Length 832;
Best Local Similarity 10.1%; Pred. No. 3.5;
Matches 35; Conservative 161; Mismatches 142; Indels 7; Gaps 1;

QY 45 CAAACTTTTACAGGCTTATCTGCTATTATCATAGACCTTCAGGCAAACTCTCTCAAG 104
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 YRWYWKYTTWYAKWTWKWSYWKYWKYWKYWKYWKYWKYWKYWKYWKYWKYWKYWKYWKY 60

QY 105 ATGATTGGCCAAACCTTCGCTGGTTTACTAGCTGCGAGACTCTGATACCAAA- 163
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 RYAMVGYKKKAMCRTLTKKKKKGYMMWYMGWRSYRNAMWTRTGTGYAYRSMYTWWR 120

QY 164 -----GATGTTCCCTGCTCGGAGGTAGTAATCCCTGGGCAATGTTACTTCTTCAAG 217
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 YRCWKXAYRYKTYCSKGTWWRWKXATTTWWKTYTWAATRYWMMCTWRWAS 180

QY 218 GACAAAGCAGATTTGCCAAAGGCAAGGACCTTTGCAATAGACTGGAAGCCAGAAATG 277
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 WYCWMMGKARKWSTWRKRSYASARSACRCCYCSGWSGMSWKYMRWRWRGWATGAGM 240

QY 278 TGTCTGAGAACGGATCTTGTGCATCTGACGGTCTGCTTTTTCAGTGGTGTGTGCT 337
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
241 KAWRASCMRRKYAGSKTSYKSMWNCWTRSWKTCYTRAWTGYCYRKGWGRGRWY 300

QY 338 GATGTTTCCATGATACAGTGTATGAGCGAGGCTCATTTTCA 382
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 ASKKYMKRWKWCWARMYRYSTGTTRASMMWRWYTTMMKWKYK 345

RESULT 15
US-09-308-375-1
; Sequence 1, Application US/09308375
; Patent No. 6300117
; GENERAL INFORMATION:
; APPLICANT: Genencor International, Inc.
; TITLE OF INVENTION: Proteases from Gram-Positive Organisms
; FILE REFERENCE: GC394-PCT
; CURRENT APPLICATION NUMBER: US/09/308,375
; CURRENT FILING DATE: 1999-05-14
; EARLIER APPLICATION NUMBER: EP9719636.4
; EARLIER FILING DATE: 1997-09-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7100
; TYPE: DNA
; ORGANISM: Bacillus subtilis
US-09-308-375-1

Query Match
  6.0%; Score 29.4; DB 4; Length 7100;
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Best Local Similarity 55.3%; Pred. No. 15;
 Matches 57; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
 QY 17 TCAGAACTGTTCCCTGAGGATCCTGGTCCAAACTTTTACAGGCTTATCTGCTATTATC 76
 Db 3418 TCAGATGCTATGCAGTTTCGATCCGTTCAAGATGCTTTAAATGGGATATTTTAAATAC 3477
 QY 77 ATAGACCTTCAGGCAAAATCCTCTCAAGGATGATTGGCCAACA 119
 Db 3478 ACCAAAGATCAAGTAGCTCCTCTCAATGATCTTCTGGAAAAA 3520

Search completed: June 25, 2004, 22:19:11
 Job time : 65 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 25, 2004, 22:05:51 ; Search time 318 Seconds
(without alignments)
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Title: US-09-773-476-294

Perfect score: 489
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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3: /cgn2_6/ptodata/1/pubpna/US05_NEW_PUB.seq:
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:
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10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
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15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	353	72.2	923	9	US-09-726-348-1
2	353	72.2	932	13	US-10-245-752-7
3	353	72.2	932	13	US-10-245-752-7
4	353	72.2	932	14	US-10-245-859-7
5	353	72.2	932	15	US-10-001-054-1
6	353	72.2	932	15	US-10-245-103-7
7	353	72.2	932	15	US-10-245-107-7
8	353	72.2	932	15	US-10-245-143-7
9	353	72.2	932	15	US-10-245-771-7
10	353	72.2	932	15	US-10-245-851-7
11	353	72.2	932	15	US-10-245-883-7
12	353	72.2	932	15	US-10-237-535-7
13	353	72.2	932	15	US-10-238-183-7
14	353	72.2	932	15	US-10-238-283-7
15	353	72.2	932	15	US-10-238-370-7

15	353	72.2	932	15	US-10-245-055-7	Sequence 7, Appli
16	353	72.2	932	15	US-10-245-147-7	Sequence 7, Appli
17	353	72.2	932	15	US-10-245-730-7	Sequence 7, Appli
18	353	72.2	932	15	US-10-245-739-7	Sequence 7, Appli
19	353	72.2	932	15	US-10-246-210-7	Sequence 7, Appli
20	353	72.2	932	15	US-10-239-196-7	Sequence 7, Appli
21	353	72.2	932	15	US-10-243-024-7	Sequence 7, Appli
22	353	72.2	932	15	US-10-243-409-7	Sequence 7, Appli
23	353	72.2	932	15	US-10-245-621-7	Sequence 7, Appli
24	353	72.2	932	15	US-10-245-880-7	Sequence 7, Appli
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26	353	72.2	932	15	US-10-243-095-7	Sequence 7, Appli
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37	353	72.2	932	15	US-10-238-325-7	Sequence 7, Appli
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42	353	72.2	932	15	US-10-243-446-7	Sequence 7, Appli
43	353	72.2	932	15	US-10-245-874-7	Sequence 7, Appli
44	353	72.2	932	15	US-10-242-653-7	Sequence 7, Appli
45	353	72.2	932	15	US-10-243-167-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-726-348-1
; Sequence 1, Application US/09726348
; Patent No. US2002025553A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: et al,
; TITLE OF INVENTION: Transforming Growth Factor Alpha HIII
; FILE REFERENCE: PF220P1
; CURRENT APPLICATION NUMBER: US/09/726,348
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 08/778,545
; PRIOR FILING DATE: 1997-01-03
; PRIOR APPLICATION NUMBER: 60/011,136
; PRIOR FILING DATE: 1996-01-04
; PRIOR APPLICATION NUMBER: 60/168,387
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 923
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-726-348-1

Query Match 72.2%; Score 353; DB 9; Length 923;
Best Local Similarity 84.0%; Pred. No. 2.5e-114;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY	4	TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGGTCCAACTTTTACAGGCTT	62
Db	222	TGGGGCTGGATCTCAGAACTGTTCTCTGGAGGACCTGGTCCAACTTTCATCAGGCAC	281
QY	63	ATATGCTATTATCATGACCTTCAGGAAATCTCTCAAGATGATTTGGCCAAACCT	122
Db	282	ATACCACTGTATCATGACCTGCAAGCAAAACCCCTCAAGGTGACTTGGCCAAACCT	341

QY 123 TCCGTGGGTTTACTCAGTGCAGACTCTGATACCTACCAAGATGTTCCCTGTCTCTGGAG 182
Db 342 TCCGTGGGTTTACTCAGTGCAGACTCTGATACCTACCAAGATGTTCCCTGTCTCTGGAG 401
QY 183 GTAGTAATGCTCGGACAACTTACTTCTTCAAGGACAGAGAGATGTTCCAAAGGGGCAA 242
Db 402 GAATTAATGCTCGAATACTATCACTCTTATATAGCAACCAATCTGTCAAGGGCAA 461
QY 243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTTCTCTGAGAACGATCTTGTGCAT 302
Db 462 AGAACCTTTGCAATAAAGCACTGGGACCCAGAAATGTTCTCTGAGATGATCTTGTGTAC 521
QY 303 CTGACGGTCTGGTCTTTTTCAGTGCCTTGTCTGATGTTTCCATGGATACAAGTGA 362
Db 522 CTGATGGTCCAGGCTTTTTCAGTGTGTTTGTCTGATGTTTCCATGGATACAAGTGA 581
QY 363 TGAGCCAGGGCTCACTTTTCACTGCTTATGTTTCTTGGGATTTCTGGATCCACACGCTAG 422
Db 582 TGGCCAGGGCTGCTTCTCACTGCTTATGTTTCTTGGGATTTCTGGAGCCACCACTCTAT 641
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Db 642 CCGTCTCCATTTCTGCTTTGGGCGACCCAGCGCCGGAAGCCAGGCTTATGAGCTTCACT 701
QY 483 AAGACTT 489
Db 702 AGGTCTT 708

RESULT 2

US-10-245-752-7
; Sequence 7, Application US/10245752
; Publication No. US20030064473A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C86
; CURRENT APPLICATION NUMBER: US/10/245,752
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116

; SEQ ID NO 7
; LENGTH: 932
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 911
; OTHER INFORMATION: unknown base
US-10-245-752-7

Query Match 72.2%; Score 353; DB 13; Length 932;
Best Local Similarity 84.0%; Pred. No. 2.5e-114;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTCTGTCCTCAAACTTTTACAGGCTT 62
Db 229 TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCTCTGTCCTCAAACTTTTATCAGGCAC 288
QY 63 ATACTGCTATTATATATAGACCTTCAGGCAAAATCTCTCAAGGATGATTGGCCCAACACT 122
Db 289 ATACCACTGTCTATATAGACCTTCAGGCAAAACCTCTCAAGGATGATTGGCCCAACACT 348
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATATACCAAGATGTTCCCTGTCTCTGGAG 182
Db 349 TCCGTGGGTTTACTCAGCTCCAGACTCTGATATGCGCAACATGTCACCTGTCTCTGGAG 408
QY 183 STAGTAATGCTGGGACAAATGTTACTTCTTCAAGGACAGCAGATTGCCAAGGGCAA 242
Db 409 GAATTAATGCTGGAAATATATACCTCTTATATAGCAACCAATCTGTCAAGGGCAA 468
QY 243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTTCTCTGAGAACGATCTTGTGCAT 302
Db 469 AGAACCTTTGCAATAAAGCACTGGGACCCAGAAATGTTCTCTGAGATGGAATCTTGTGTAC 528
QY 303 CTGACGGTCTCTGCTTTTTCAGTGCCTTTTGTCTGATGTTTCCATGGATACAAGTGA 362
Db 529 CTGATGGTCCAGGCTTTTTCAGTGTGTTTGTCTGATGTTTCCATGGATACAAGTGA 588
QY 363 TGAGGACAGGCTCACTTTTCACTGCTTATGTTCTTGGGATTTCTGGATCCACACGCTAG 422
Db 589 TGGCCAGGGCTGTTCTCACTGCTTATGTTCTTGGGATTTCTGGAGCCACCTCTAT 648
QY 423 CCATCTNCACTTCTACTTTGGGAACCCAGCGCCGGAAGCCAGGCTTATGAGCCACAC 482
Db 649 CCGTCTCCATTTCTGCTTTGGGCGACCCAGCGCCGGAAGCCAGGCTTATGAGCTAT 708
QY 483 AAGACTT 489
Db 709 AGGTCTT 715

RESULT 3

US-10-245-859-7
; Sequence 7, Application US/10245859
; Publication No. US20030064474A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C78
; CURRENT APPLICATION NUMBER: US/10/245,859
; CURRENT FILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 10/197942
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/065027
PRIOR FILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/086478
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090689
PRIOR FILING DATE: 1998-08-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 7
LENGTH: 932
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: unsure
LOCATION: 911
OTHER INFORMATION: unknown base
US-10-245-859-7

Query Match 72.2%; Score 353; DB 13; Length 932;
Best Local Similarity 84.0%; Pred. No. 2.5e-114; Mismatches 0; Indels 1; Gaps 1;
Matches 409; Conservative 77;
4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCTTGGTCCAACTTTTACAGGTT 62
229 TGGGCTGGATCTCAGAACTGTTCTGGAGGACCTGGTCCAACTTTTACAGGAC 289
63 ATACTGCTATTATCATAGACCTTCAGGAATTCCTCTCAAGATGATTTGGCCACACT 122
289 ATACCACCTGTCATCATAGACCTGCAAGCAACCCCTCAAAGTGACTTGGCCACACT 348
123 TCCGTGGTGTACTCAGCTGCAGACTCTGATCTACCAAGATGTTCCCTGCTCTGGAG 182
349 TCCGTGGTGTACTCAGCTGCAGACTCTGATCTACCAAGATGTTCCCTGCTCTGGAG 408
183 SPAGTAATGCTGGGACAAATGTTACTTCTTCAAGGACAAAGCAGATTTGCCAAGGGCAA 242
409 GAATTAATGCTGGGAACTATCACTCTTATATAGAACCAAAATCTGTCAAGGGCAA 468
243 GGGACCTTGGCAATAGCACTGGAAGCCAGAAATGTCTCTGAGAACGATCTGTGCAAT 302
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363 TGAGGAGGCTCATTTTCACTGCTATGTTCTTTGGGATCTGGGATCCACGCTAG 422
589 TCGGCGAGGCTCGTTCTCACTGCTATGTTCTTGGGATCTGGGATCCACGCTAT 648
423 CCATCTCATCTTACTTTGGGAAACCCAGCGCCGGAAGGCTTATGAGCCACAC 482
649 CGTCTCATCTGTTTGGGAAACCCAGCGCCGGAAGGCTTATGAGCCACAC 708
483 AAGACTT 489
709 AGGTCTT 715

RESULT 4
US-10-001-054-1
Sequence 1, Application US/10001054
Publication No. US20020192209A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Baker, Kevin
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Hebert, Carolyn
APPLICANT: Hensel, William
APPLICANT: Kabakoff, Rhona
APPLICANT: Shelton, David
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
FILE OF INVENTION: CELL GROWTH
FILE REFERENCE: P3034R1PCT
CURRENT APPLICATION NUMBER: US/10/001,054
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/088858
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/096891
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/096894
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PRIOR FILING DATE: 1999-06-22
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PRIOR FILING DATE: 1999-06-23

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PRIOR FILING DATE: 1999-07-20
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PRIOR FILING DATE: 1999-10-29
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PRIOR FILING DATE: 2000-03-03
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PRIOR FILING DATE: 1999-04-12
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PRIOR FILING DATE: 1999-08-25
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PRIOR APPLICATION NUMBER: 09/872035
PRIOR FILING DATE: 2001-06-01
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PRIOR APPLICATION NUMBER: 09/924419
PRIOR FILING DATE: 2001-08-06
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PRIOR FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 09/941992
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: 09/946374
PRIOR FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: PCT/US98/18824
PRIOR FILING DATE: 1998-09-10
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PRIOR APPLICATION NUMBER: PCT/US99/05028
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PRIOR APPLICATION NUMBER: PCT/US99/08615
PRIOR FILING DATE: 1999-04-20
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PRIOR FILING DATE: 1999-09-01
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PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR FILING DATE: 1999-12-20
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PRIOR FILING DATE: 2000-01-06
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: PCT/US00/04341
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PRIOR FILING DATE: 2000-02-18
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PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: PCT/US00/06884
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: PCT/US00/13705
PRIOR FILING DATE: 2000-05-17
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PRIOR FILING DATE: 2000-05-22
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PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17800
PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: PCT/US01/19692
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: PCT/US01/21066
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: PCT/US01/27099
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 1
LENGTH: 932
TYPE: DNA
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: unsure
LOCATION: 911
OTHER INFORMATION: unknown base

Query Match 72.2%; Score 353; DB 14; Length 932;
Best Local Similarity 84.0%; Pred. No. 2.5e-114; Indels 1; Gaps 1;
Matches 409; Conservative 0; Mismatches 77;
QY 4 TGAGGCTAGATCTTTCAGAACTGTTCCCT-GAGGATCTCTGTCCAACTTTTACAGCTT 62
Db 229 TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCTGTGTCACAACTTTTCATCAGGCAC 288
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAATCCTCTCAAGGATGATTTCGCCAACACCT 122
Db 289 ATACCACTGTTCATCATAGACCTTCAGGCAACCTTCCTCAAGGATGATTTCGCCAACACCT 348
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACTACCAAGATGTTCCCTGTCTCTGGAG 182
Db 349 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACTACCAAGATGTTCCCTGTCTCTGGAG 408

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QY 183 GTAGTAATGCTGGACAAATGTTACTTTTCAAGCAAGCAGATTTGCCAAGGGCAA 242
Db 409 GAAATTAATGCTGGAAATCTATCACTCTTATATAGCAACCAAACTGTCAAGGGCAA 468
QY 243 GGGACCTTTGCAATAGCACTGGAGCCAGAAATGTCCTGAGAACGGATCTTGCGAT 302
Db 469 AGAACCTTTGCAATAGCACTGGAGCCAGAAATGTCCTGAGAACGGATCTTGCGAT 528
QY 303 CTGACGGCTCTGCTTTTTCAGTCTGCTTTGCTGCTGATGGTTTCCATGGATACAAAGTGA 362
Db 529 CTGATGGTCCAGGCTCTTTGCAATAGCACTGGAGCCAGAAATGTCCTGAGAACGGATCTTGCGAT 588
QY 363 TGAGCAGGGCTCAATTTCACTGCTTATGCTTTTGGGATCTGGATCCACCGCTAG 422
Db 589 TCGGCAGGGCTCGTTCTCACTGCTTATGCTTTTGGGATCTGGATCCACCGCTAT 648
QY 423 CCATCTNCATTTACTTTGGGAAACCCAGCGCGGAAAGCAAGGCTTTCATGAGCCAC 482
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QY 483 AAGACTT 489
Db 709 AGGTCTT 715

RESULT 5
US-10-245-103-7
; Sequence 7, Application US/10245103
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C112
; CURRENT APPLICATION NUMBER: US/10/245,103
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 7
; LENGTH: 932
; TYPE: DNA
; ORGANISM: Homo Sapien
```

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; FEATURE:
; NAME/KEY: unsure
; LOCATION: 911
; OTHER INFORMATION: unknown base
US-10-245-103-7

Query Match 72.2%; Score 353; DB 15; Length 932;
Best Local Similarity 84.0%; Pred. No. 2.5e-114;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGGTCCAAACTTTTTCACAGGCTT 62
Db 229 TGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCTTGTCCAAACTTTCATCAGGCAC 288
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAAACTCTTCAAGAGATGATTTGGCCAAACACT 122
Db 289 ATACCAGTGTATCATAGACCTTCAGGCAAACTCTTCAAGAGTGTACTTGGCCAAACACT 348
QY 123 TCCGTGGTGTACTCAGCTGCAGACTGTGATCTACTACCAAGATGTTCCCTGTCTGGAG 182
Db 349 TCCGTGGCTTTACTCAGCTCCAGACTGTGATCTGCCAACATGTCACTGTCTCTGGAG 408
QY 183 GTAGTAATGCTGGGACAATGTTACTTTTCAAGGACAAGCAGATTTGCCAAGGGCAA 242
Db 409 GAAATTAATGCTGGAAATCTATCACTCTTATATAGCAACCAAACTGTCAAGGGCAA 468
QY 243 GGGACCTTTGCAATAGCACTGGAGCCAGAAATGTCCTGAGAACGGATCTTGCGAT 302
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QY 303 CTGACGGCTCTGCTTTTTCAGTCTGCTTTGCTGCTGATGGTTTCCATGGATACAAAGTGA 362
Db 529 CTGATGGTCCAGGCTCTTTGCAATAGCACTGGAGCCAGAAATGTCCTGAGAACGGATCTTGCGAT 588
QY 363 TGAGCAGGGCTCAATTTCACTGCTTATGCTTTTGGGATCTGGATCCACCGCTAG 422
Db 589 TCGGCAGGGCTCGTTCTCACTGCTTATGCTTTTGGGATCTGGATCCACCGCTAT 648
QY 423 CCATCTNCATTTACTTTGGGAAACCCAGCGCGGAAAGCAAGGCTTTCATGAGCCAC 482
Db 649 CGGTCTCCATTTCTGTTGGGCGACCCAGCGCGGAAAGCAAGGCTTTCATGAGCCAC 708
QY 483 AAGACTT 489
Db 709 AGGTCTT 715

RESULT 6
US-10-245-107-7
; Sequence 7, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C71
; CURRENT APPLICATION NUMBER: US/10/245,107
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/063046
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/065027
 ; PRIOR FILING DATE: 1997-11-10
 ; PRIOR APPLICATION NUMBER: 60/079689
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/086478
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087607
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/089801
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/090557
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090689
 ; PRIOR FILING DATE: 1998-06-25
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 116
 ; SEQ ID NO 7
 ; LENGTH: 932
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: 911
 ; OTHER INFORMATION: unknown base
 US-10-245-107-7

Query Match 72.2%; Score 353; DB 15; Length 932;
 Best Local Similarity 84.0%; Pred. No. 2.5e-114;
 Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

Qy	4	TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGTCACAACTTTTACAGGCTT	62
Db	229	TGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTCACAACTTTTCATCAGGCAC	288
Qy	63	ATAGTGTATATATAGACCTTCAGCAAACTCTCAAGATGATTTGGCCCAACCT	122
Db	289	ATACCACTGTATATAGACCTTCAGCAAACTCTCAAGATGATTTGGCCCAACCT	348
Qy	123	TCGCTGGTCTTACTCAGCTCAGACTCTGATATACCAAGATGTTCCCTGCTGGAG	182
Db	349	TCGCTGGTCTTACTCAGCTCAGACTCTGATATACCAAGATGTTCCCTGCTGGAG	408
Qy	183	GTAGTAATGCTGGCAATGTTACTTCTTCAAGCAACAGAGATTTGCCAAGGGCAA	242
Db	409	GAATTAATGCTGGCAATGTTACTTCTTCAAGCAACAGAGATTTGCCAAGGGCAA	468
Qy	243	GGGACCTTTGCAATAGACCTTCAGCAAACTCTCAAGATGATTTGCCAAGGGCAA	302
Db	469	AGAACCTTTGCAATAGACCTTCAGCAAACTCTCAAGATGATTTGCCAAGGGCAA	528
Qy	303	CTGACGCTCTGCTCTTTTTCAGTGGTGTGCTGATGTTTCCATGGATACCAAGTGA	362
Db	529	CTGATGCTCAGGCTCTTTTCAGTGGTGTGCTGATGTTTCCATGGATACCAAGTGA	588
Qy	363	TGAGCAGGCTCATTTTCTACTGTTTCTTGGATCTGGATCCACACGCTAG	422
Db	589	TGCGCAGGCTCGTCTCTACTGTTTCTTGGATCTGGATCCACACGCTAG	648
Qy	423	CCATCTNCATCTTACTTTGGGGAACCCAGCGCCGGAAGCCAGGCTTTCATGAGCCACAC	482
Db	649	CCGCTCCATCTTCTTTTGGGGAACCCAGCGCCGGAAGCCAGGCTTTCATGAGCTACAT	708
Qy	483	AGAGCTT	489
Db	709	AGGCTTT	715

RESULT 7
 US-10-245-143-7
 ; Sequence 7, Application US/10245143
 ; Publication No. US20030068780A1

; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Stephan, Jean-Phillippe
 ; APPLICANT: Watanabe, Colin
 ; APPLICANT: Wood, William
 ; APPLICANT: Zhang, Zemin
 ; APPLICANT: Fong, Sherman
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3630R1C90
 ; CURRENT APPLICATION NUMBER: US/10/245,143
 ; CURRENT FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: 10/197942
 ; PRIOR FILING DATE: 2002-07-18
 ; PRIOR APPLICATION NUMBER: 60/059114
 ; PRIOR FILING DATE: 1997-09-17
 ; PRIOR APPLICATION NUMBER: 60/063046
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/065027
 ; PRIOR FILING DATE: 1997-11-10
 ; PRIOR APPLICATION NUMBER: 60/079689
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/086478
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087607
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/089801
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: 60/090557
 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090689
 ; PRIOR FILING DATE: 1998-06-25
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 116
 ; SEQ ID NO 7
 ; LENGTH: 932
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: 911
 ; OTHER INFORMATION: unknown base
 US-10-245-143-7

Query Match 72.2%; Score 353; DB 15; Length 932;
 Best Local Similarity 84.0%; Pred. No. 2.5e-114;
 Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

Qy	4	TGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGTCACAACTTTTACAGGCTT	62
Db	229	TGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTCACAACTTTTCATCAGGCAC	288
Qy	63	ATAGTGTATATATAGACCTTCAGCAAACTCTCAAGATGATTTGGCCCAACCT	122
Db	289	ATACCACTGTATATAGACCTTCAGCAAACTCTCAAGATGATTTGGCCCAACCT	348
Qy	123	TCGCTGGTCTTACTCAGCTCAGACTCTGATATACCAAGATGTTCCCTGCTGGAG	182
Db	349	TCGCTGGTCTTACTCAGCTCAGACTCTGATATACCAAGATGTTCCCTGCTGGAG	408
Qy	183	GTAGTAATGCTGGCAATGTTACTTCTTCAAGCAACAGAGATTTGCCAAGGGCAA	242
Db	409	GAATTAATGCTGGCAATGTTACTTCTTCAAGCAACAGAGATTTGCCAAGGGCAA	468
Qy	243	GGGACCTTTGCAATAGACCTTCAGCAAACTCTCAAGATGATTTGCCAAGGGCAA	302
Db	469	AGAACCTTTGCAATAGACCTTCAGCAAACTCTCAAGATGATTTGCCAAGGGCAA	528

QY 303 CTGACGGTCCGGTCTTTTGCAGTGGCTTTGTGCTGATGGTTTCCATGGATACAAGTGTA 362
Db 529 CTGATGGTCCAGGCTTTTGCAGTGTGTTGTGCTGATGGTTTCCATGGATACAAGTGTA 588
QY 363 TGAGCAGGGTCAATTTCACTGCTTATGTTCTTTGGGATCTGGGATCCACCAAGCTAG 422
Db 589 TGGCCAGGGTCTGTTCTCACTGCTTATGTTCTTTGGGATCTGGGATCCACCAAGCTAT 648
QY 423 CCATCTNCATTCTACTTTGGGAAACCCAGCGCCGGAAGCCAAAGCTTATGAGCCACAC 482
Db 649 CGTCTCCATTCTGTTTGGGCGCCAGCGCCGGAAGCCAAAGCTTATGAGCTACAT 708
QY 483 AAGACTT 489
Db 709 AGGTCTT 715

RESULT 8

US-10-245-771-7
; Sequence 7, Application US/10245771
; Publication No. US20030068781A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C98
; CURRENT APPLICATION NUMBER: US/10/245,771
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 7
; LENGTH: 932
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 911
; OTHER INFORMATION: unknown base
US-10-245-771-7

Query Match

72.2%; Score 353; DB 15; Length 932;

Best Local Similarity 84.0%; Pred. No. 2.5e-114;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCTT-CAGGATCCTGGTCCAAACTTTTACAGGCTT 62
Db 229 TGGGGCTGGATCTCCAGAACTGTTCCTTCTGGAGACCTGTCTCCAAACTTTTCACTAGGAC 288
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCCAACACCT 122
Db 289 ATACCCTGTGTCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCCAACACCT 348
QY 123 TCGTGGGTTTACTTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGTCTGGAG 182
Db 349 TCCGTGGCTTTACTTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGTCTGGAG 408
QY 183 GTAGTATGCTGGGCAATGTTACTTCTTTCAGGCAAGCAGATTTGCCAGGGGCAA 242
Db 409 GAATTAATGCTGGAATACCTATCACCTCTTATATAGAACCCAAATCTGTCAAGGGGCAA 468
QY 243 GGGACCTTTGCAATAGCACTGGAAAGCCAGAAATGTCTCTGAGAAACGGATCTTGTGCAT 302
Db 469 AGAACCTTTGCAATAGCACTGGGACCCAGAAATGTCTCTGAGAAATGGATCTTGTGTAC 528
QY 303 CTGACGGTCTCTGTTTTCAGTGGGTTTGTCTGATGGTTTCCATGGATACAAGTGTA 362
Db 529 CTGATGGTCCAGGTCTTTTGCAGTGTGTTTGTCTGATGGTTTCCATGGATACAAGTGTA 588
QY 363 TGAGGCGAGGCTCATTTTTCAGTCTTATGTTCTTTCGGATCTTGGGATCCACCAAGCTAG 422
Db 589 TGGCCAGGCTGTTCTCTCACTTAATGTTCTTTCGGATCTTGGGATCCACCAAGCTAT 648
QY 423 CCATCTNCATTCTACTTTGGGAAACCCAGCGCCGGAAGCCAAAGCTTATGAGCCACAC 482
Db 649 CGTCTCCATTCTGTTTGGGCGCCAGCGCCGGAAGCCAAAGCTTATGAGCTACAT 708
QY 483 AAGACTT 489
Db 709 AGGTCTT 715

RESULT 9

US-10-245-851-7
; Sequence 7, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C93
; CURRENT APPLICATION NUMBER: US/10/245,851
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478

; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 7
; LENGTH: 932
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 911
; OTHER INFORMATION: unknown base
US-10-245-851-7

Query Match 72.2%; Score 353; DB 15; Length 932;
Best Local Similarity 84.0%; Pred. No. 2.5e-114;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-CAGGATCTCTGGTCCAAACTTTTACAGGCTT 62
DB 229 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTCTCCAACTTTCATCAGGCAC 288
QY 63 ATACTGCTATTATCATAGACCTTCAGCAAAATCTCTCAAGGATGATTTGGCCAAACCT 122
DB 289 ATACCACCTGTCTCATAGACCTGCAAGCAAAACCCCTCAAAGTGACTTGGCCAAACCT 348
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGATGTTCCCTGTCTGGAG 182
DB 349 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGATGTTCCCTGTCTGGAG 408
QY 183 GTAGTAATGCTGGCAATGTTACTTCTTCAAGGACAGAGATTTGCCAAGGCCAAA 242
DB 409 GAATTAATGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTCTCCAACTTTCATCAGGCAC 468
QY 243 GGGACCTTTGCAATAGACCTGGAAGCCAGAAATGTTCTCTGAGACGGATCTTGTGCAT 302
DB 469 AGAACCTTTGCAATAAACACTGGGACCCAGAAATGTTCTCTGAGATGGATCTTGTGTAC 528
QY 303 CTGACGGTCTCTGTTCTTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATCAAGTGTA 362
DB 529 CTGATGCTCCAGGCTCTCTCTACTGTTCTCTGATGTTCTCTGATGTTTCCATGGATCAAGTGTA 588
QY 423 CCATCTNCAATCTACTTTTGGGGAACCCAGCCCGGAAAGCCAGGCTTTCATGAGCCACAC 482
DB 649 CCGTCTCCATCTCTGTTTGGGCGACCCAGCCCGGAAAGCCAGGCTTTCATGACTACAT 708
QY 483 AAGACTT 489
DB 709 AGGTCTT 715

RESULT 10
US-10-245-883-7
; Sequence 7, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Fillvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin

; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3830R1C70
; CURRENT APPLICATION NUMBER: US/10/245.883
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 7
; LENGTH: 932
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 911
; OTHER INFORMATION: unknown base
US-10-245-883-7

Query Match 72.2%; Score 353; DB 15; Length 932;
Best Local Similarity 84.0%; Pred. No. 2.5e-114;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
QY 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-CAGGATCTCTGGTCCAAACTTTTACAGGCTT 62
DB 229 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTCTCCAACTTTCATCAGGCAC 288
QY 63 ATACTGCTATTATCATAGACCTTCAGCAAAATCTCTCAAGGATGATTTGGCCAAACCT 122
DB 289 ATACCACCTGTCTCATAGACCTGCAAGCAAAACCCCTCAAAGTGACTTGGCCAAACCT 348
QY 123 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGATGTTCCCTGTCTGGAG 182
DB 349 TCCGTGGGTTTACTCAGCTGCAGACTCTGATCTACCAAGATGTTCCCTGTCTGGAG 408
QY 183 GTAGTAATGCTGGCAATGTTACTTCTTCAAGGACAGAGATTTGCCAAGGCCAAA 242
DB 409 GAATTAATGCTGGATCTCCAGAACTGTTCTCTGGAGACCTGTCTCCAACTTTCATCAGGCAC 468
QY 243 GGGACCTTTGCAATAGACCTGGAAGCCAGAAATGTTCTCTGAGACGGATCTTGTGCAT 302
DB 469 AGAACCTTTGCAATAAACACTGGGACCCAGAAATGTTCTCTGAGATGGATCTTGTGTAC 528
QY 303 CTGACGGTCTCTGTTCTTTTTCAGTGGGTTTGTCTGATGTTTCCATGGATCAAGTGTA 362
DB 529 CTGATGCTCCAGGCTCTCTCTACTGTTCTCTGATGTTTCCATGGATCAAGTGTA 588
QY 363 TGAGGCGAGGCTCATTTTCTCTACTGTTTGTCTGATGTTTCCATGGATCAAGTGTA 422

Db 589 TCGCCAGGGCTCGTTCTCACTGTTATGTTCTCGGATTCTGGAGCCACTCTAT 648
QY 423 CCATCTCATCTACTTTTGGGAACCCAGCGCGGAAAGCCAAAGCTTATGAGCCAC 482
Db 649 CGCTCCATTCTGTTTGGGACCCAGCGCGGAAAGCCAAAGCTTATGAGACTACAT 708
QY 483 AAGACTT 489
Db 709 AGGTCTT 715

RESULT 11
US-10-237-535-7
; Sequence 7, Application US/10237535
; Publication No. US20030073188A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630RIC3
; CURRENT APPLICATION NUMBER: US/10/237,535
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091358
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-09-10
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; PRIOR FILING DATE: 1998-11-03
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; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119342
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/123957
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123972
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: 60/127372
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/131271
; PRIOR FILING DATE: 1999-04-27

; PRIOR APPLICATION NUMBER: 60/133459
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/135725
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/135729
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138385
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/140653
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144732
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/144790
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145228
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146843
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/148188
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/148513
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/149327
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149395
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/150114
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/151700
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/151734
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/177118
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: 60/179851
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 60/180921
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/187202
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/198587
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 60/199614
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/206330
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/206368
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/209832
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/218371
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/222695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/229896
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/230621
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/232887

1	PRIOR FILING DATE: 2000-09-15	
2	PRIOR APPLICATION NUMBER: 60/235147	
3	PRIOR FILING DATE: 2000-09-22	
4	PRIOR APPLICATION NUMBER: 60/261878	
5	PRIOR FILING DATE: 2001-01-12	
6	PRIOR APPLICATION NUMBER: 60/261910	
7	PRIOR FILING DATE: 2001-01-16	
8	PRIOR APPLICATION NUMBER: 60/261939	
9	PRIOR FILING DATE: 2001-01-16	
10	PRIOR APPLICATION NUMBER: 60/262150	
11	PRIOR FILING DATE: 2001-01-16	
12	PRIOR APPLICATION NUMBER: 60/264395	
13	PRIOR FILING DATE: 2001-01-25	
14	PRIOR APPLICATION NUMBER: 60/266421	
15	PRIOR FILING DATE: 2001-02-02	
16	PRIOR APPLICATION NUMBER: 60/267623	
17	PRIOR FILING DATE: 2001-02-09	
18	PRIOR APPLICATION NUMBER: 60/274399	
19	PRIOR FILING DATE: 2001-03-09	
20	PRIOR APPLICATION NUMBER: 60/280982	
21	PRIOR FILING DATE: 2001-04-03	
22	PRIOR APPLICATION NUMBER: 60/282129	
23	PRIOR FILING DATE: 2001-04-04	
24	PRIOR APPLICATION NUMBER: 60/282199	
25	PRIOR FILING DATE: 2001-04-04	
26	PRIOR APPLICATION NUMBER: 60/290589	
27	PRIOR FILING DATE: 2001-05-09	
28	PRIOR APPLICATION NUMBER: 09/180997	
29	PRIOR FILING DATE: 1998-11-19	
30	PRIOR APPLICATION NUMBER: 09/267213	
31	PRIOR FILING DATE: 1999-03-12	
32	PRIOR APPLICATION NUMBER: 09/380137	
33	PRIOR FILING DATE: 1999-08-25	
34	PRIOR APPLICATION NUMBER: 09/380138	
35	PRIOR FILING DATE: 1999-08-25	
36	PRIOR APPLICATION NUMBER: 09/403297	
37	PRIOR FILING DATE: 1999-10-18	
38	PRIOR APPLICATION NUMBER: 09/423741	
39	PRIOR FILING DATE: 1999-11-10	
40	PRIOR APPLICATION NUMBER: 09/709238	
41	PRIOR FILING DATE: 2000-11-08	
42	PRIOR APPLICATION NUMBER: 09/802706	
43	PRIOR FILING DATE: 2001-03-09	
44	PRIOR APPLICATION NUMBER: 09/872035	
45	PRIOR FILING DATE: 2001-06-01	
46	PRIOR APPLICATION NUMBER: 09/918585	
47	PRIOR FILING DATE: 2001-07-30	
48	PRIOR APPLICATION NUMBER: 09/924419	
49	PRIOR FILING DATE: 2001-08-06	
50	PRIOR APPLICATION NUMBER: 09/927796	
51	PRIOR FILING DATE: 2001-08-09	
52	PRIOR APPLICATION NUMBER: 09/929404	
53	PRIOR FILING DATE: 2001-08-13	
54	PRIOR APPLICATION NUMBER: 09/931836	
55	PRIOR FILING DATE: 2001-08-16	
56	PRIOR APPLICATION NUMBER: 09/941992	
57	PRIOR FILING DATE: 2001-08-28	
58	PRIOR APPLICATION NUMBER: 09/946374	
59	PRIOR FILING DATE: 2001-09-04	
60	PRIOR APPLICATION NUMBER: 10/001054	
61	PRIOR FILING DATE: 2001-11-30	
62	PRIOR APPLICATION NUMBER: 10/052586	
63	PRIOR FILING DATE: 2002-01-15	
64	PRIOR APPLICATION NUMBER: 10/081056	
65	PRIOR FILING DATE: 2002-02-20	
66	PRIOR APPLICATION NUMBER: 10/119480	
67	PRIOR FILING DATE: 2002-04-09	

Query Match 72.2%; Score 353; DB 15; Length 932;
Best Local Similarity 84.0%; Pred. No. 2.5e-114;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
4 TCAGGCTAGATCTTCAGACATGTTCCCT-GAGGATCTCGGTCCAACTTTTACAGGCTT 62

Db	229	TGGGGTGGATCTCAGAACTGTCTCTGGAGGACCTGTGTCAAACTTTTCATCAGGCAC	122
Qy	63	ATATCTGCTATTATCATAGACCTTCAGGCAAAATCCTCTCAAGGATGATTTGGCCAAACACCT	182
Db	289	ATACCACTGCTCATCATAGACCTTGCAGACAAACCCCTCAAGGTGACTTGGCCAAACACCT	348
Qy	123	TCGTGGGTTTACTCAGCTGCAGACTCTGTATCTACACAAGATGTTCCCTGTCCTGGAG	182
Db	349	TCGTGGCTTTTACTCAGACTCCAGACTCTGTATCTGCCACAACATGTCAACTGTCTCTGGAG	408
Qy	183	GTAGTAATGCGCTGGGACAAATGTTACTCTTTCAAAGGACAAAGCAGATTTGCCAAGGGCAAA	242
Db	409	GAATTAATGCGCTGGAACTACTATCACCTCTTATATAGACACCAAAATCTGTCAAGGGCAAA	468
Qy	243	GGGACCTTTGCAATAGCACTCGAAAGCCAGCAAAATGTGTCTCTGAGAACGGATCTTTGTCAT	302
Db	469	AGAAACCTTTGCAATAACACTGGGACCCAGCAAAATGTGTCTCTGAGAATGGATCTTTGTGTAC	528
Qy	303	CTGACGGTCTGCTCTTTTGCAGTCCGTTTGTGCTGATGTTTCCATGGATACAAGTGTA	362
Db	529	CTGATGCTCCAGGCTCTTTTGCAGTGTGTTGTGCTGATGTTTCCATGGATACAAGTGTA	588
Qy	363	TGAGGCAGGGCTCATTTTCACTGCTTATGTTTCTTTGGGATTTCTGGGATCCACCACGCTAG	422
Db	589	TGGCCAGGGCTCGTTCTCACTGCTTATGTTTCTTCGGGATTTCTGGGAGCCACCACCTTAT	648
Qy	423	CCATCTNCAATCTACTTTTGGGGAACCCAGCGCCGGAAGCAAGGCTTATGAGCCACAC	482
Db	649	CCGCTCTCAATCTGCTTTTGGGCGAACCCAGCGCCGGAAGCAAGGCTTATGAGCCACAC	708
Qy	483	AAAGACTT 489	
Db	709	AGGTCTT 715	

RESULT 12

US-10-238-183-7

; Sequence 7, Application US/10238183

; Publication No. US20030073189A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Eaton, Dan

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Goddard, Audrey

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Phillippe

; APPLICANT: Watanabe, Colin

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; APPLICANT: Fong, Sherman

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3630R111

; CURRENT APPLICATION NUMBER: US/10/238,183

; CURRENT FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: 10/197942

; PRIOR FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/059114

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/063046

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/065027

; PRIOR FILING DATE: 1997-11-10

; PRIOR APPLICATION NUMBER: 60/079689

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: 60/086478

; PRIOR FILING DATE: 1998-05-22

; PRIOR APPLICATION NUMBER: 60/087607

; PRIOR FILING DATE: 1998-06-02

; PRIOR APPLICATION NUMBER: 60/089801

, PRIOR FILING DATE: 1998-06-18
, PRIOR APPLICATION NUMBER: 60/090557
, PRIOR FILING DATE: 1998-06-24
, PRIOR APPLICATION NUMBER: 60/090689
, PRIOR FILING DATE: 1998-06-25
, PRIOR APPLICATION NUMBER: 60/091358
, PRIOR FILING DATE: 1998-07-01
, PRIOR APPLICATION NUMBER: 60/091978
, PRIOR FILING DATE: 1998-07-07
, PRIOR APPLICATION NUMBER: 60/099803
, PRIOR FILING DATE: 1998-09-10
, PRIOR APPLICATION NUMBER: 60/106932
, PRIOR FILING DATE: 1998-11-03
, PRIOR APPLICATION NUMBER: 60/115554
, PRIOR FILING DATE: 1999-01-12
, PRIOR APPLICATION NUMBER: 60/119342
, PRIOR FILING DATE: 1999-02-09
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, PRIOR FILING DATE: 1999-07-26
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, PRIOR FILING DATE: 1999-07-28
, PRIOR APPLICATION NUMBER: 60/146843
, PRIOR FILING DATE: 1999-08-03
, PRIOR APPLICATION NUMBER: 60/148188
, PRIOR FILING DATE: 1999-08-10
, PRIOR APPLICATION NUMBER: 60/148513
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, PRIOR APPLICATION NUMBER: 60/170262
, PRIOR FILING DATE: 1999-12-09
, PRIOR APPLICATION NUMBER: 60/177118
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, PRIOR FILING DATE: 2000-02-02
, PRIOR APPLICATION NUMBER: 60/180921
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, PRIOR APPLICATION NUMBER: 60/187202
, PRIOR FILING DATE: 2000-03-03
, PRIOR APPLICATION NUMBER: 60/198587
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, PRIOR FILING DATE: 2000-09-15
, PRIOR APPLICATION NUMBER: 60/235147
, PRIOR FILING DATE: 2000-09-22
, PRIOR APPLICATION NUMBER: 60/261878
, PRIOR FILING DATE: 2001-01-12
, PRIOR APPLICATION NUMBER: 60/261910
, PRIOR FILING DATE: 2001-01-16
, PRIOR APPLICATION NUMBER: 60/261939
, PRIOR FILING DATE: 2001-01-16
, PRIOR APPLICATION NUMBER: 60/262150
, PRIOR FILING DATE: 2001-01-16
, PRIOR APPLICATION NUMBER: 60/264395
, PRIOR FILING DATE: 2001-01-25
, PRIOR APPLICATION NUMBER: 60/266421
, PRIOR FILING DATE: 2001-02-02
, PRIOR APPLICATION NUMBER: 60/267623
, PRIOR FILING DATE: 2001-02-09
, PRIOR APPLICATION NUMBER: 60/274399
, PRIOR FILING DATE: 2001-03-09
, PRIOR APPLICATION NUMBER: 60/280982
, PRIOR FILING DATE: 2001-04-03
, PRIOR APPLICATION NUMBER: 60/282129
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, PRIOR APPLICATION NUMBER: 60/282199
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, PRIOR APPLICATION NUMBER: 60/290589
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, PRIOR FILING DATE: 1999-03-12
, PRIOR APPLICATION NUMBER: 09/380137
, PRIOR FILING DATE: 1999-08-25
, PRIOR APPLICATION NUMBER: 09/380138
, PRIOR FILING DATE: 1999-08-25
, PRIOR APPLICATION NUMBER: 09/403297
, PRIOR FILING DATE: 1999-10-18
, PRIOR APPLICATION NUMBER: 09/423741
, PRIOR FILING DATE: 1999-11-10
, PRIOR APPLICATION NUMBER: 09/709238
, PRIOR FILING DATE: 2000-11-08
, PRIOR APPLICATION NUMBER: 09/802706
, PRIOR FILING DATE: 2001-03-09
, PRIOR APPLICATION NUMBER: 09/872035
, PRIOR FILING DATE: 2001-06-01
, PRIOR APPLICATION NUMBER: 09/918585
, PRIOR FILING DATE: 2001-07-30
, PRIOR APPLICATION NUMBER: 09/924419

```

1  APPLICANT: Stephan, Jean-Phillippe
2  APPLICANT: Watanabe, Colin
3  APPLICANT: Wood, William
4  APPLICANT: Zhang, Zemin
5  APPLICANT: Fong, Sherman
6  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
7  TITLE OF INVENTION: ACIDS ENCODING THE SAME
8  FILE REFERENCE: P3630R1C15
9  CURRENT APPLICATION NUMBER: US/10/238,283
10 CURRENT FILING DATE: 2002-09-09
11 PRIOR APPLICATION NUMBER: 10/197942
12 PRIOR FILING DATE: 2002-07-18
13 PRIOR APPLICATION NUMBER: 60/059114
14 PRIOR FILING DATE: 1997-09-17
15 PRIOR APPLICATION NUMBER: 60/063046
16 PRIOR FILING DATE: 1997-10-24
17 PRIOR APPLICATION NUMBER: 60/065027
18 PRIOR FILING DATE: 1997-11-10
19 PRIOR APPLICATION NUMBER: 60/079689
20 PRIOR FILING DATE: 1998-03-27
21 PRIOR APPLICATION NUMBER: 60/086478
22 PRIOR FILING DATE: 1998-05-22
23 PRIOR APPLICATION NUMBER: 60/087607
24 PRIOR FILING DATE: 1998-06-02
25 PRIOR APPLICATION NUMBER: 60/089801
26 PRIOR FILING DATE: 1998-06-18
27 PRIOR APPLICATION NUMBER: 60/090557
28 PRIOR FILING DATE: 1998-06-24
29 PRIOR APPLICATION NUMBER: 60/090689
30 PRIOR FILING DATE: 1998-06-25
31 Remaining Prior Application data removed - See File Wrapper or PALM.
32 NUMBER OF SEQ ID NOS: 116
33 SEQ ID NO 7
34 LENGTH: 932
35 TYPE: DNA
36 ORGANISM: Homo Sapien
37 FEATURE:
38 NAME/KEY: unsure
39 LOCATION: 911
40 OTHER INFORMATION: unknown base
41 US-10-238-283-7

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RESULT 13
US-10-238-283-7
; Sequence 7, Application US/10238283
; Publication No. US20030073190A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria

QY 423 CCATCTNCACTTCTACTTTGGGGAACCCAGCGCCGGAAGCCAGGCTTATGAGCCAC 482
Db 649 CCGTCTCCATCTGCTTTGGGCGACCCAGCGCCGGAAGCCAGGCTTATGAGCCAC 708
QY 483 AAGACTT 489
Db 709 AGGTCTT 715

RESULT 14
US-10-238-370-7
; Sequence 7, Application US/10238370
; Publication No. US20030073192A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C10
; CURRENT APPLICATION NUMBER: US/10/238,370
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 7
; LENGTH: 932
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 911
; OTHER INFORMATION: unknown base
US-10-238-370-7

Query Match 72.2%; Score 353; DB 15; Length 932;
Best Local Similarity 84.0%; Pred. No. 2.5e-114;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;

QY 4 TGAGGCTAGACTTTCAGAACTTTCCT-GAGATCCTGGTCCAACTTTTACAGGCTT 62
Db 229 TGGGGCTGAGCTTCCAGAACTTTCCTGGAGGACCCCTGGTCCAACTTTCATCAGGCAC 288
QY 63 ATACTGCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTGGCCACACT 122

Db 289 ATACCACCTGTCATATAGACCTTGAAGCAAAACCCCTCAAAGGTGACTTTGGCCAAACACT 348
QY 123 TCGGTGGGTTTACTTCAGCTGCAGACTCTGATATACCAACAAGATGTTCCCTGTCCTGGAG 182
Db 349 TCGGTGGCTTTACTCAGCTCCAGACTCTGATCTGCCACAACATGTCACACTGTCCTGGAG 408
QY 183 GTAGTAATGCTGGGACAATGTTACTTCTTCAAGGACAAGCAGATTTGCCAAGGGGCAAA 242
Db 409 GAATTAATGCTGGAATATCTATCACCTCTTATATAGACCAACCAATCTGTCAAGGGGCAAA 468
QY 243 GGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCTCTGAGAACGGGATCTTGTGCAT 302
Db 469 AGAACCTTTGCAATATACACTGGGGACCCAGAAATGTCTCTGAGAAATGGATCTTGTGTAC 528
QY 303 CTGACGGTCTCTGCTTTTTCAGTGGCTTGTGCTGATGCTTTCATGGATACAAGTGA 362
Db 529 CTGATGCTCCAGGCTCTTTTGCAGTGTGTTTGTCTGATGCTTTCATGGATACAAGTGA 588
QY 363 TGAGGCAGGCTCATTTTCACTGCTTATGTTCTTTCGGATTTCTGGGATCCACCACGCTAG 422
Db 589 TGGCCAGGCTCTGTTCTCACTGCTTATGTTCTTTCGGATTTCTGGGATCCACCACGCTAT 648
QY 423 CCATCTNCACTTCTACTTTGGGAAACCCAGCGCCGGAAGCCAGGCTTATGAGCCACAC 482
Db 649 CCGTCTCCATCTGCTTTGGGCGACCCAGCGCCGGAAGCCAGGCTTATGAGCTATCAT 708
QY 483 AAGACTT 489
Db 709 AGGTCTT 715

RESULT 15
US-10-245-055-7
; Sequence 7, Application US/10245055
; Publication No. US20030073192A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C88
; CURRENT APPLICATION NUMBER: US/10/245,055
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689

PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116

; SEQ ID NO 7

; LENGTH: 932

; TYPE: DNA

; ORGANISM: Homo Sapien

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 911

; OTHER INFORMATION: unknown base

US-10-245-055-7

Query Match 72.2%; Score 353; DB 15; Length 932;
Best Local Similarity 84.0%; Pred. No. 2.5e-114;
Matches 409; Conservative 0; Mismatches 77; Indels 1; Gaps 1;
Qy 4 TGAGGCTAGATCTTCAGAACTGTTCCCT-CAGGATCCTGGTCCAAACTTTTACAGGCTT 62
Db 229 TGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCTGGTCCAAACTTTCATCAGGCAC 288
Qy 63 ATACTGCTATTATCATAGACTTCAGGCAAACTCTCTCAGAGATGATTTGGCCAAACACT 122
Db 289 ATACCACTGTCTCATAGACTTCAGGCAAACTCTCTCAGAGATGATTTGGCCAAACACT 348
Qy 123 TCGTGGGTTTACTCAGCTCAGACTCTGATCTTACCAAGATGTTCCCTGTCTGGAG 182
Db 349 TCGTGGCTTTACTCAGCTCAGACTCTGATCTTACCAAGATGTTCCCTGTCTGGAG 408
Qy 183 GTAGTAATGCTGGCAATGTTACTTCTTTCAAGGACAGCAGATTTCAGGCAAA 242
Db 409 GAATTAATGCTGGCAATGTTACTTCTTTCAAGGACAGCAGATTTCAGGCAAA 468
Qy 243 GGGACCTTTGCAATAGCACTGGAAGCCGCAAAATGTTCTGTGAGACGGATCTTGTGCAT 302
Db 469 AGAACCTTTGCAATAGCACTGGAAGCCGCAAAATGTTCTGTGAGATGGATCTTGTGTAC 528
Qy 303 CTGACGCTCCTGGTCTTTTTCAGTGGCTTTTGTGCTGATGTTTCCATGGATCAAGTGA 362
Db 529 CTGATGCTCCAGGCTTTTTCAGTGGCTTTTGTGCTGATGTTTCCATGGATCAAGTGA 588
Qy 363 TGAGGAGGCTCATTTTCTACTGCTTATGTTCTTTGGGATCTGGGATCCACACCTAG 422
Db 589 TGGCCAGGCTCGTCTCTACTGCTTATGTTCTTCGGGATCTGGGAGCCACCTCTAT 648
Qy 423 CCATCTNCAATCTACTTTGGGAAACCCAGCCCGGAAAGCCAGGCTTATGAGCCACAC 482
Db 649 CCGTCTCCATCTGCTTTGGGAGCCAGCCCGGAAAGCCAGGCTTATGAGCCACAC 708
Qy 483 AAGACTT 489
Db 709 AGGTCTT 715

Search completed: June 25, 2004, 23:37:51
Job time : 320 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 25, 2004, 09:08:52 ; Search time 54 Seconds
(without alignments)
5117.249 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 888
Sequence: 1 gactgagctagattcttag.....tntatgacacacaagactt 489

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 3172214

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO.spool_P/US09773476/runat_25062004_090846_5808/app_query.fasta_1.647
-DB=A_Geneseq_25Jan04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NCM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09773476 -CCN_1_181 -runat_25062004_090846_5808 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCGAPOP=6
-FCGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_29Jan04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	690	77.7	229	2 AAW27087	Aaw27087 Human tra
2	690	77.7	229	2 AAY05282	Aay05282 EGF-like
3	690	77.7	229	2 AAY13944	Aay13944 Human tra
4	690	77.7	229	3 AAB33419	Aab33419 Human PRO
5	690	77.7	229	3 AAY88570	Aay88570 Human PRO
6	690	77.7	229	3 AAB50951	Aab50951 Human PRO
7	690	77.7	229	4 AAU04295	Aau04295 Transform
8	690	77.7	229	4 AAB20112	Aab20112 Human imm
9	690	77.7	229	4 AAB68595	Aab68595 PRO240_4
10	690	77.7	229	5 AAM51083	Aam51083 Human tra

11	690	77.7	229	5 ABG34033	ABg34033 Human PRO
12	690	77.7	229	6 ABU71417	ABu71417 Human neo
13	690	77.7	229	6 ADA01276	ADa01276 Human PRO
14	690	77.7	229	6 ADA43705	ADa43705 Human sec
15	690	77.7	229	6 ADA43473	ADa43473 Human sec
16	690	77.7	229	6 ADA01148	ADa01148 Human PRO
17	690	77.7	229	7 ADA01032	ADa01032 Human sec
18	690	77.7	229	7 ADA43589	ADa43589 Human sec
19	690	77.7	229	7 ADA06851	ADa06851 Human PRO
20	690	77.7	229	7 ADA08339	ADa08339 Novel hum
21	690	77.7	229	7 ADB99632	ADb99632 Human PRO
22	690	77.7	229	7 ADB86915	ADb86915 Human PRO
23	690	77.7	229	7 ADB66070	ADb66070 Human sec
24	690	77.7	229	7 ADB99748	ADb99748 Human PRO
25	690	77.7	229	7 ADB99403	ADb99403 Novel hum
26	690	77.7	229	7 ADB65954	ADb65954 Human sec
27	690	77.7	229	7 ADC23352	ADc23352 Human tra
28	690	77.7	229	7 ADC26045	ADc26045 Human PRO
29	690	77.7	229	7 ADE04872	ADe04872 Human PRO
30	690	77.7	229	7 ADE11178	ADe11178 Human PRO
31	690	77.7	229	7 ADD88109	ADd88109 Human PRO
32	690	77.7	229	7 ADD95404	ADd95404 Human sec
33	690	77.7	229	7 ADE06334	ADe06334 Human PRO
34	690	77.7	229	7 ADE38109	ADe38109 Human PRO
35	690	77.7	229	7 ADD88225	ADd88225 Human PRO
36	690	77.7	229	7 ADD90806	ADd90806 Human sec
37	690	77.7	229	8 ADE51659	ADe51659 Human sec
38	690	77.7	229	8 ADE51775	ADe51775 Human sec
39	690	77.7	229	8 ADE37633	ADe37633 Human sec
40	690	77.7	229	8 ADE37517	ADe37517 Human sec
41	690	77.7	229	8 ADD95288	ADd95288 Human sec
42	690	77.7	229	8 ADE37988	ADe37988 Human PRO
43	690	77.7	229	8 ADE76077	ADe76077 Human PRO
44	690	77.7	229	8 ADE39400	ADe39400 Human PRO
45	690	77.7	229	8 ADE04204	ADe04204 Human PRO

ALIGNMENTS

RESULT 1
AAW27087
ID AAW27087 standard; protein; 229 AA.
XX

AC	AAW27087;	
DT	28-JAN-1998 (first entry)	
DE	Human transforming growth factor alpha HIII.	
XX	human transforming growth factor; TGF; TGF-alpha-HIII; angiogenesis;	
KW	embryogenesis; ocular disorder; kidney disorder; liver disorder;	
KW	neural disorder; alopecia; inflammation.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Region	1..177
FT		/label= soluble_portion_of_protein
FT	Peptide	1..25
FT		/label= signal_peptide
FT		/note= "putative"
FT	Protein	26..229
FT		/label= mature_protein
FT	Region	126..177
FT		/label= active_site
FT	Region	178..204
FT		/label= transmembrane_portion
FT		/note= "putative"
XX	WO9725349-A1.	
PD	17-JUL-1997.	
XX		

PF 04-JAN-1996; 96WO-US000149.
 XX
 PR 04-JAN-1996; 96WO-US000149.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Wei Y;
 XX
 DR WPI: 1997-372817/34.
 DR N-PSDB; AAT85082.
 XX
 PT New human transforming growth factor-alpha homologue - used for
 PT developing products for treating e.g. neurological disorders, kidney and
 PT liver disorders, tumours, wounds, hair loss or skin disorders.
 XX
 XX
 PS Claim 15; Page 47; 63pp; English.
 CC This protein has been putatively identified as a human transforming
 CC growth factor (TGF) alpha analogue, TGF-alpha-HIII. The protein can
 CC stimulate angiogenesis, embryogenesis, cell differentiation and function.
 CC It can be used for therapeutic purposes for restoration or enhancement of
 CC neurological functions diminished as a result of trauma or other damaging
 CC pathologies such as AIDS dementia and senile dementia, to treat ocular
 CC disorders, e.g. corneal inflammation, to destroy target cells, to treat
 CC tumours, kidney or liver disorders or to treat wounds, burns or ulcers.
 CC The polypeptide can also be used in the modulation of angiogenesis, bone
 CC resorption, immune response, and synaptic and neuronal effector
 CC functions, or the arachidonic acid cascade. It can also be used in
 CC applications related to terminal differentiation e.g. in
 CC hyperproliferative disorders such as inflammation or psoriasis and for
 CC alopecia, hair loss or other skin conditions which affect hair follicular
 CC development. Antagonists to TGF-alpha-HIII can be used for treating
 CC tumours or skin disorders such as psoriasis. The products can also be
 CC used for diagnosis and detection of the above disorders
 XX
 SQ Sequence 229 AA;
 Alignment Scores:
 Pred. NO.: 4.61e-63 Length: 229
 Score: 690.00 Matches: 128
 Percent Similarity: 89.68% Conservativity: 11
 Best Local Similarity: 82.58% Mismatches: 16
 Query Match: 77.70% Indels: 1
 Gaps: 0
 DB: 2

US-09-773-476-294 (1-489) x AAW27087 (1-229)

QY 3 CTGAGGCTAGATCTTCAGAACTGTCCT-GAGGATCCTGCTCAAACTTTTACAGGCT 61
 DB 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
 QY 62 TATACTGCTATATCATAGACCTTCAGGCAAACTCCTCAAGATGATTGGCCACACC 121
 DB 93 HisThrThrValIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
 QY 122 TTCGCTGGGTTTACTCAGCTCAGACTGTGATATACCAAGATGTCCTGCTCTGGA 181
 DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132
 QY 182 GGTAGTAAATGCTGGGCAATGTTACTTCTTTCAGGACCAAGCAGATTTCCCAAGGGCAA 241
 DB 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGln 152
 QY 242 AGGACCTTTCATAGACTGGAGCCGAGATGTCCTGAGACGGATCTTGCA 301
 DB 153 LysAsnLeuCysAsnAsnThrGlyAspProGlyMetCysProGluAsnGlySerCysVal 172
 QY 302 TCTCAGCGTCTCGTCTTTTTCAGTGGGTTTGTCTGCTGATGTTTCCATGATCAAGTGT 361
 DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192
 QY 362 ATGAGGAGGGCTCATTTTCTACTGCTTATGTTCTTTTGGATTCTGGGATCCACACGCTA 421

DB 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
 QY 422 GCCATCTNCATCTTACTTTGGGACCCAGCGCCGGAAGCCAAAG 466
 DB 213 SerValSerIleLeuLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227
 RESULT 2
 AAY05282
 ID AAY05282 standard; protein; 229 AA.
 XX
 AC AAY05282;
 XX
 DT 22-JUN-1999 (first entry)
 XX
 DE EGF-like homologue PRO240.
 XX
 KW Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;
 KW BBAP-2; inhibitor; tumour growth; cancer; EGF-like homologue;
 KW FGF-8 homologue.
 OS Homo sapiens.
 PN WO9914327-A2.
 XX
 PD 25-MAR-1999.
 XX
 PF 10-SEP-1998; 98WO-US018824.
 XX
 PR 17-SEP-1997; 97US-0059114P.
 PR 17-SEP-1997; 97US-0059117P.
 PR 18-SEP-1997; 97US-0059263P.
 PR 15-OCT-1997; 97US-0062125P.
 PR 17-OCT-1997; 97US-0062285P.
 PR 17-OCT-1997; 97US-0062287P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 25-NOV-1997; 97US-0066840P.
 XX
 XX (GETH) GENENTECH INC.
 PA Botstein D, Goddard A, Gurney A, Hillan X, Lawrence DA, Roy M;
 PI Wood WI;
 XX
 DR WPI: 1999-229532/19.
 DR N-PSDB; AAX28432.
 XX
 PT Antibodies against specific proteins overexpressed in tumors.
 XX
 PS Example 1; Fig 12; 130pp; English.
 XX
 CC This sequence represents the EGF-like homologue PRO240. The invention
 CC relates to antibodies (Ab) that bind to any of the polypeptides (I)
 CC designated PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246
 CC or BBAP-2. The Ab, or other agents that inhibit expression and/or
 CC activity of (I) are used: (i) to inhibit growth of tumours; and (ii) as
 CC diagnostic/prognostic reagents for detection or quantification of (I) in
 CC cells or tissues, by standard immunoassays, with overexpression being
 CC indicative of cancer. For therapeutic use, the Ab may be conjugated to a
 CC toxin, chemotherapeutic agent or radioisotope. Genes expressing (I), many
 CC of which are growth factor homologues, are overexpressed in some cases of
 CC cancer
 XX
 SQ Sequence 229 AA;
 Alignment Scores:
 Pred. NO.: 4.61e-63 Length: 229
 Score: 690.00 Matches: 128
 Percent Similarity: 89.68% Conservativity: 11
 Best Local Similarity: 82.58% Mismatches: 16
 Query Match: 77.70% Indels: 1
 Gaps: 0
 DB: 2

US-09-773-476-294 (1-489) x AAY05282 (1-229)

CC be useful as carcinostatic agents or as antigens for preparing antibodies
 CC against the proteins. The cDNAs can be used as probes for gene diagnosis
 CC and gene sources for gene therapy, as well as for large-scale expression
 CC of the proteins. The HP01498 (see AAY13939) protein may be associated
 CC with signal transduction associated with apoptosis, and therefore useful
 CC in inhibition of apoptosis. The HP01962 (see AAY13943) protein can be
 CC used to treat diseases associated with phosphatidylethanolamine N-
 CC methyltransferase. The proteins are identified by the presence of a
 CC hydrophobic transmembrane region, knowledge of the protein function is
 CC not required, as in e.g. methods of expression cloning

XX
 SQ Sequence 229 AA;

Alignment Scores:
 Pred. No.: 4,61e-63 Length: 229
 Score: 690.00 Matches: 128
 Percent Similarity: 89.68% Conservatives: 11
 Best Local Similarity: 82.58% Mismatches: 16
 Query Match: 77.70% Indels: 1
 DB: 2 Gaps: 0

US-09-773-476-294 (1-489) x AAY13944 (1-229)

QY 3 CTGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGTCACAACTTTTACAGGCT 61
 DB 73 LeuGlyLeuAspLeuGlnAsnProGlyProAsnPheHisGlnAla 92
 QY 62 TATACGTCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTGGCCAAACACC 121
 DB 93 HisThrThrValIleleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
 QY 122 TTCGCTGGGTTTACTCAGCTGCAGACTCTGATACCAAGAGATGTTCCCTGCTCTGGA 181
 DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132
 QY 182 GGTAGTAATGCTGGGCAATGTTACTTCTTCAAGGACAGCAGATTTGCCAAGGGCAA 241
 DB 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrlleAspAsnGlnIleCysGlnGlyGln 152
 QY 242 AGGACCTTTGCAATAGACCTGGAAGCCAGCAATGTCTCTGAGACGAGATCTTTGTCGA 301
 DB 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
 QY 302 TCTGACGGTCTGCTGTTTGGGCAATGTTGCTGATGTTTCCATGGATACCAAGTGT 361
 DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrllysCys 192
 QY 362 ATGAGCAGGCTCATTTTCACTCTCTATGTTCTTTGGGATTTCTGGATCCACCGCTA 421
 DB 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
 QY 422 GCCATCTNCATCTTACTTGGGAAACCCAGCCGCGGAAAGCCAG 466
 DB 213 SerValSerIleLeuLeuTrpAlaThrGlnArgGlyLysAlaLys 227

RESULT 4
 AAB33419
 ID AAB33419 standard; protein; 229 AA.
 XX
 AC AAB33419;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO240 protein UNQ214 SEQ ID NO:26.
 XX
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
 KW antianaemic; hepatotropic; virucide; antipariatic; antiallergic;
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;

QY 3 CTGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGTCACAACTTTTACAGGCT 61
 DB 73 LeuGlyLeuAspLeuGlnAsnProGlyProAsnPheHisGlnAla 92
 QY 62 TATACGTCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTGGCCAAACACC 121
 DB 93 HisThrThrValIleleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
 QY 122 TTCGCTGGGTTTACTCAGCTGCAGACTCTGATACCAAGAGATGTTCCCTGCTCTGGA 181
 DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132
 QY 182 GGTAGTAATGCTGGGCAATGTTACTTCTTCAAGGACAGCAGATTTGCCAAGGGCAA 241
 DB 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrlleAspAsnGlnIleCysGlnGlyGln 152
 QY 242 AGGACCTTTGCAATAGACCTGGAAGCCAGCAATGTCTCTGAGACGAGATCTTTGTCGA 301
 DB 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
 QY 302 TCTGACGGTCTGCTGTTTGGGCAATGTTGCTGATGTTTCCATGGATACCAAGTGT 361
 DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrllysCys 192
 QY 362 ATGAGCAGGCTCATTTTCACTCTCTATGTTCTTTGGGATTTCTGGATCCACCGCTA 421
 DB 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
 QY 422 GCCATCTNCATCTTACTTGGGAAACCCAGCCGCGGAAAGCCAG 466
 DB 213 SerValSerIleLeuLeuTrpAlaThrGlnArgGlyLysAlaLys 227

RESULT 4
 AAB33419
 ID AAB33419 standard; protein; 229 AA.
 XX
 AC AAB33419;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 DE Human PRO240 protein UNQ214 SEQ ID NO:26.
 XX
 KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
 KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
 KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
 KW antianaemic; hepatotropic; virucide; antipariatic; antiallergic;
 KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
 KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
 KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
 KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;

Human transmembrane proteins and nucleotide sequences.

Claim 1; Page 90-91; 139pp; English.

This sequence is a human transmembrane protein of the invention. All of the proteins exist in the cell membrane, so are considered to be proteins controlling the proliferation and differentiation of the cells. They may

autoimmune thrombocytopaenia; immune-mediated renal disease;
 CC denvyelinating disease; hepatobiliary disease; Whipple's disease;
 CC inflammatory bowel disease; gluten-sensitive enteropathy;
 CC autoimmune disease; immune-mediated skin disease; allergic disease;
 CC immunological disease; transplantation associated disease;
 CC graft rejection; graft-versus-host-disease.

OS Homo sapiens.

XX WO200053758-A2.

XX 14-SEP-2000.

XX 02-MAR-2000; 2000WO-US005841.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1999; 99US-0123618P.

XX 12-MAR-1999; 99US-0123957P.

XX 23-MAR-1999; 99US-0125775P.

XX 12-APR-1999; 99US-0128849P.

XX 20-APR-1999; 99WO-US008615.

XX 28-APR-1999; 99US-0131445P.

XX 04-MAY-1999; 99US-0132371P.

XX 14-MAY-1999; 99US-0134287P.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 28-JUL-1999; 99US-0146222P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020394.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 05-OCT-1999; 99WO-US023089.

XX 29-OCT-1999; 99US-0162506P.

XX 29-NOV-1999; 99WO-US028214.

XX 30-NOV-1999; 99WO-US028313.

XX 30-NOV-1999; 99WO-US028409.

XX 01-DEC-1999; 99WO-US028301.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 02-DEC-1999; 99WO-US028564.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030999.

XX 30-DEC-1999; 99WO-US031274.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000277.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

XX 22-FEB-2000; 2000WO-US004414.

(GETH) GENENTECH INC.

XX Askenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;

XX Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;

XX Stewart TA, Tunas D, Watanabe CK, Wood WI, Yan M;

XX WPI; 2000-572271/53.

XX N-PSDB; AAC58584.

XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

XX Claim 33; Fig 12; 309pp; English.

XX The present invention describes sixty four human PRO proteins which can
 CC be used in the treatment of immune related diseases. The human PRO
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for

CC treating and diagnosing immune related disorders. The disorders are
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
 CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
 CC immune-mediated renal disease, demyelinating diseases of the central and
 CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
 CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
 CC or immune-mediated skin diseases, allergic diseases, immunological
 CC diseases of the lung, and transplantation associated diseases including
 CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
 CC represent PCR primers and hybridisation probes used in the isolation of
 CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
 CC represent human PRO polynucleotide and protein sequences given in the
 CC exemplification of the present invention

XX Sequence 229 AA;

XX Alignment Scores:

Pred. No.:	4.61e-63	Length:	229
Score:	690.00	Matches:	128
Percent Similarity:	89.68%	Conservative:	11
Best Local Similarity:	82.58%	Mismatches:	16
Query Match:	77.70%	Indels:	1
DB:	3	Gaps:	0

US-09-773-476-294 (1-489) x AAB33419 (1-229)

QY	3	CTGAGGCTAGATCTTCAGAACTGTTCCCT-CAGGATCCTGGTCCAACTTTTACAGGCT	61
DB	73	LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPhHisGlnAla	92
QY	62	TATACGTCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCAAACC	121
DB	93	HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr	112
QY	122	TTCCGTGGTTCACAGCTGACACTCTGATACCTACCAAGATGTTCCCTGCTCTGGA	181
DB	113	PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly	132
QY	182	GGTAGTAATGCTGGGACAATGTTACTTCTTCAAGGACACAGCAGATTTGCCAAGGCAA	241
DB	133	GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln	152
QY	242	AGGACCTTTTCATAGCAGCTGGAAGCCAGAAATGTCTCTGAGACGATCTTGTGCA	301
DB	153	LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal	172
QY	302	TCTGACGCTCTGCTGCTTTTCAGTGGCTTTGTCTGATGTTTCCATGGATCAAGTGT	361
DB	173	ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys	192
QY	362	ATGAGCGAGGCTCATTTTTCATGCTTATGTTCTTGGATTCCTGGATCCACCGCTA	421
DB	193	MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu	212
QY	422	GCCATCTNCATCTTACTTTGGGACCCAGCGCGGAAGCCAAAG	466
DB	213	SerValSerIleLeuLeuTrpAlaThrGlnArgLysAlaLys	227

RESULT 5

AA58570

ID AA58570 standard; protein; 229 AA.

XX AA58570;

AC AA58570;

XX 09-AUG-2000 (first entry)

DT 09-AUG-2000 (first entry)

XX Human PRO240 amino acid sequence.

XX Antibody; PRO187; PRO533; PRO214; PRO240; PRO211; PRO230; PRO261; PRO246;

KW PRO317; tumour growth inhibitor; cancer; diagnosis; treatment; human;

KW cell growth proliferation; serrate precursor; C-serrate-1; ADEPT;
XX antibody dependent enzyme mediated prodrug therapy; chromosome 2.
XX

OS Homo sapiens.

PN WO200015665-A2.

XX 23-MAR-2000.

PF 08-SEP-1999; 99WO-US020594.

XX 10-SEP-1998; 98US-0099803P.

PR 10-SEP-1998; 98WO-US018824.

XX (GETH) GENENTECH INC.

XX Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WI, Botstein D;
XX WPI; 2000-271386/23.

DR N-PSDB; AAA30036.

XX New isolated antibodies which bind to specific polypeptides used for
PT diagnosis and treatment of neoplastic cell growth and proliferation.
XX

XX Example 4; Fig 8; 200pp; English.

XX This sequence represents a human PRO240 amino acid sequence. PRO240
CC shares sequence homology with the D. melanogaster serrate precursor
CC protein and the Gallus gallus C-serrate-1 protein. The PRO240 gene is
CC located on chromosome 2. The invention relates to isolated antibodies
CC which bind to a polypeptide. The "PRO" polypeptides are encoded by genes
CC which are over expressed in the genome of tumour cells. Vectors and host
CC cells comprising the nucleic acid encoding the antibodies are used in the
CC production of the antibodies. The antibodies and nucleic acids encoding
CC them are used for diagnosing a tumour in a mammal. The antibodies are
CC used for inhibiting the growth of tumour cells and identifying compounds
CC that inhibit a biological or immunological activity of and/or expression
CC of a PRO187, PRO533, PRO214, PRO240, PRO211, PRO230, PRO261, PRO246 or
CC PRO317 polypeptide. The antibody can be used in antibody dependent enzyme
CC mediated prodrug therapy (ADEPT) by conjugating the antibody to a prodrug
CC -activating enzyme which converts a prodrug to an anti-cancer drug. The
CC antibodies can be fluorescently labelled and monitored by light
CC microscopy, flow cytometry or fluorimetry for diagnosis and prognosis of
CC tumours

XX SQ Sequence 229 AA;

Alignment Scores:

Pred. No.: 4 61e-63 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 3 Gaps: 0

US-09-773-476-294 (1-489) x AAY88570 (1-229)

QY 3 CTGAGCTAGACTTCAGAACTGTCCTT- GAGGATCTCGTCCAACTTTTACAGCT 61
DB 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
QY 62 TATAGTCTATTATCATAGACTTCAGCAATCTCTCAAGGATGATTGGCCCAACACC 121
DB 93 HisThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
QY 122 TTCGGTGGGTTTACTCAGCTGCAGACTCTGATCTACTACCAAGATGTTCCCTGCTGGA 181
DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132
QY 182 GTAGTAGTCCCTGGACATGTTACTTCTTCAGGACAGACAGATTTGCCAGGGCAA 241
DB 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGln 152

QY 242 AGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCCTGAGAACGAGTCTTGCA 301
DB 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
QY 302 TCTGACGCTCCTGCTCTTTTGCAGTGGTGTGCTGATGCTTCCATGATACAAGTGT 361
DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192
QY 362 ATGAGCGAGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGGATCCACCGCTA 421
DB 193 MetArgGlnGlySerPheSerLeuLeuMetPheGlyIleLeuGlyAlaThrThrLeu 212
QY 422 GCCATCTNCATTTCTACTTTGGGAAACCCAGCGCCGAAAGCCAAAG 466
DB 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227

RESULT 6

AAB50951 ID AAB50951 standard; protein; 229 AA.

XX AAB50951;

XX 21-MAR-2001 (first entry)

XX Human PRO240 protein.

XX Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
XX antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
XX PRO agonist; cancer; inflammatory disorder; immunological disorder.

XX Homo sapiens.

XX WO200073348-A2.

XX 07-DEC-2000.

XX 30-MAY-2000; 2000WO-US014941.

XX 02-JUN-1999; 99WO-US012252.

XX 22-JUN-1999; 99US-0140650P.

XX 23-JUN-1999; 99US-0141017P.

XX 20-JUL-1999; 99US-0144758P.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 29-OCT-1999; 99US-0162506P.

XX 30-NOV-1999; 99WO-US028313.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 09-DEC-1999; 99US-0170262P.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030399.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 03-MAR-2000; 2000WO-US005841.

XX 10-MAR-2000; 2000WO-US006319.

XX 15-MAR-2000; 2000WO-US006884.

XX 30-MAR-2000; 2000WO-US008439.

XX 17-MAY-2000; 2000WO-US013705.

XX (GETH) GENENTECH INC.

XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
XX Shelton D, Smith V, Watanabe CK, Wood WI;
XX WPI; 2001-016509/02.
XX N-PSDB; AAC91553.

XX Twenty eight nucleic acids encoding PRO polypeptides which are useful for
PT treating various tumors, e.g. breast cancer, and other inflammatory,
PT angiogenic and immunological disorders.

XX PS Claim 31; Fig 2; 188pp; English.

XX CC The present sequence is one of twenty eight novel P50 polypeptides. The

XX CC PRO polypeptides and their agonists, including antibodies, peptides, and

XX CC small molecule agonists, may be used to treat various tumours, e.g.,

XX CC cancers such as breast cancer, ovarian cancer, renal cancer, colorectal

XX CC cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,

XX CC central nervous system cancer, melanoma or leukaemia. They are also

XX CC useful for treating other disorders such as neuronal, glial, astrocytal,

XX CC hypothalamic and other glandular, macrophagal, epithelial, stromal and

XX CC biastocelic disorders, and inflammatory, angiogenic and immunological

XX CC disorders

XX SQ Sequence 229 AA;

Alignment Scores:

Pred. No.:	4.61e-63	Length:	229
Score:	690.00	Matches:	128
Percent Similarity:	89.68%	Conservative:	11
Best Local Similarity:	82.58%	Mismatches:	16
Query Match:	77.70%	Indels:	1
DB:	4	Gaps:	0

US-09-773-476-294 (1-489) x AAB50951 (1-229)

QY 3 CTGAGGCTAGATCTTCAGACTGTTCCCT-GAGGATCTGCTCCAACTTTTACAGGCT 61

DB 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92

QY 62 TATACTCTCTATTATCATAGACCTTCAGGCAAACTCTCAAGGATGATTGGCCACACC 121

DB 93 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuGlyAspLeuAlaThr 112

QY 122 TTCGGTGGTTACTACAGTCGACACTCTGATACCTACCAAGATGTTCCCTGTCCTGGA 181

DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132

QY 182 GGTAGTAACTCCCTGGCAATGTTACTCTTTCAAGGACAGAGATTTGCCAAGGCCAA 241

DB 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrlleAspAsnGlnIleCysGlnGlyGln 152

QY 242 AGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCCTGAGAACGATCTTGTGCA 301

DB 153 LysAsnLeuGlyCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172

QY 302 TCTGAGGTCCTGGTCTTTTTCAGTCGGTGTGCTGATGTTTCCATGATGATCAAGTGT 361

DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrllysCys 192

QY 362 ATGAGGAGGAGGCTCATTTTCACTGCTATGTTCTTTGGGATCTGGATCCACGCTA 421

DB 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212

QY 422 GCATCTNCACTTACTTTGGGAACTCCAGCGCGCGGAAAGCCAAAG 466

DB 213 SerValSerIleLeuLeuTrpAlaThrGlnArgAlaGlyAlaLys 227

RESULT 7

AAU04295

ID AAU04295 standard; protein; 229 AA.

XX AC AAU04295;

XX DT 24-OCT-2001 (first entry)

XX DE Transforming growth factor (TGF) alpha HIII.

XX KW Human; TGF alpha HIII; transforming growth factor alpha HIII; cancer;

XX KW diagnostic; therapeutic; immune disorder; multiple sclerosis;

XX KW systemic lupus erythematosus; human immuno-deficiency virus; HIV;

XX KW hyperproliferative disorder; Gaucher's disease; cardiovascular disease;

XX KW Scimitar syndrome; Chaga's cardiomyopathy; coronary arteriosclerosis;

XX KW angiogenic disorder; corneal graft; neovascularisation; wound healing;

XX KW diabetic retinopathy; neurological disorder; Huntington's chorea;

XX KW Alzheimer's disease; Parkinson's disease.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..25

FT Protein 26..229

FT Active-site 126..177

FT Region 178..204

FT /note= "Transmembrane region"

XX PN WO200140251-A1.

XX PD 07-JUN-2001.

XX PF 01-DEC-2000; 2000WO-US032745.

XX PR 02-DEC-1999; 99US-0168387P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Wei Y;

XX DR WPI; 2001-441480/47.

XX DR N-PSDB; AAS08543.

XX PT Nucleic acid encoding human transforming growth factor alpha III (TGPa),

XX PT useful for preventing, diagnosing and/or treating e.g. Cancer and

XX PT Parkinson's disease.

XX PS Claim 11; Fig 1; 302pp; English.

XX CC The sequence represents the amino acid sequence of human transforming

XX CC growth factor (TGF) alpha HIII. TGF alpha HIII nucleic acid and protein

XX CC may be used in the prevention, diagnosis and treatment of diseases

XX CC associated with inappropriate polypeptide expression, for example immune

XX CC disorders (e.g. multiple sclerosis, systemic lupus erythematosus and

XX CC human immuno-deficiency virus (HIV) infections), hyperproliferative

XX CC disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases

XX CC (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary

XX CC arteriosclerosis), angiogenic disorders (e.g. corneal graft

XX CC neovascularisation and diabetic retinopathy), neurological disorders

XX CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease),

XX CC infectious diseases and/or for promoting wound healing, regeneration

XX CC and/or chemotaxis (full details given in specification). Additionally,

XX CC the nucleic acid may be used to produce the secreted polypeptides, by

XX CC inserting the nucleic acids into a host cell and culturing the cell to

XX CC express the protein. It may also be used as a DNA probe in diagnostic

XX CC assays to detect and quantitate the presence of similar nucleic acid

XX CC sequences in samples, and therefore which patients may be in need of

XX CC restorative therapy. The polypeptides may also be used as antigens in the

XX CC production of antibodies against TGF alpha HIII and in assays to identify

XX CC modulators of TGF alpha HIII. The anti-TGF alpha HIII antibodies may also

XX CC be used as diagnostic agents for detecting the presence of TGF alpha HIII

XX CC in samples (e.g. by enzyme linked immunosorbant assay (ELISA))

XX SQ Sequence 229 AA;

Alignment Scores:

Pred. No.:	4.61e-63	Length:	229
Score:	690.00	Matches:	128
Percent Similarity:	89.68%	Conservative:	11
Best Local Similarity:	82.58%	Mismatches:	16
Query Match:	77.70%	Indels:	1
DB:	4	Gaps:	0

US-09-773-476-294 (1-489) x AAU04295 (1-229)

QY 3 CTGAGGCTAGATCTTCAGACTGTTCCCT-GAGGATCTGCTCCAACTTTTACAGGCT 61

Db 73 LeuGlyLeuAspLeuGlnAsnCySerLeuGluAspProGlyProAsnPhelGlnAla 92
Qy 62 TATACCTGCTATTATCATAGACCTTCAGGCAAAATCCTCTCAAGGATGATTGGCCCAACACC 121
Db 93 HisThrThrValIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
Qy 122 TTCGGTGGGTTTACTCAGCTGAGACTGTGATCTACTACCAAGATGTTCCCTGTCCTGGA 181
Db 113 PheA-rgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCyProGly 132
Qy 182 GGTAGTAAATGCTGGGCAAAATGTTACTTCTTTCAGGACAAAGCAGATTGCAAGGGCAA 241
Db 133 GlyIleAsnAlaTAsnThrIleThrSerTyIleAspAsnGlnIleCysGlnGlyGln 152
Qy 242 AGGACCTTTCAGTACGAGCCAGCAAAATGTTCTGAGAACGATCTTGTGCA 301
Db 153 LysAsnLeuCyAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
Qy 302 TCTGACGGTCCGCTTTTTCAGTGGCTTCTGCTGATGTTTCCATGGATACAAAGTGT 361
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrlsCys 192
Qy 362 ATGAGCGAGGCTATTTTCACTGCTTATGTTCTTGGGATCTGGGATCCACCAAGCTA 421
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
Qy 422 GCATCTCATCTACTTGGGACCCAGCCGCGGAAAGCAAG 466
Db 213 SerValSerIleLeuLeuThrAlaThrGlnArgGlyAlaLys 227

RESULT 8
AAB20112
ID AAB20112 standard; protein; 229 AA.
AC AAB20112;
XX
DT 30-APR-2001 (first entry)
XX
DE Human immunostimulant PRO240.
XX
KW PRO240; UNQ214; human; immune disease; autoimmune disease; antirheumatic;
KW antarthritic; antiinflammatory; antianaemic; immunosuppressive;
KW antihydroid; antidiabetic; neuroprotective; hepatotropic; virucide;
KW dermatological; antipsoriatic; antiasthmatic; antiallergic;
KW immunostimulant; serrate; lung cancer.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..30 /label= Signal_peptide
FT Modified-site 7..13 /note= "N-myristoylation site"
FT Modified-site 24..30 /note= "N-myristoylation site"
FT Protein 31..229 /note= "N-myristoylation site"
FT Modified-site 40..46 /label= Mature_protein
FT Modified-site 44..48 /note= "N-myristoylation site"
FT Modified-site 70..76 /note= "Asn is N-glycosylated"
FT Modified-site 79..83 /note= "N-myristoylation site"
FT Modified-site 132..138 /notes "Asn is N-glycosylated"
FT Modified-site 157..161 /note= "N-myristoylation site"
FT Modified-site 168..172 /note= "Asn is N-glycosylated"
FT Modified-site 177..183 /note= "Asn is N-glycosylated"

FT Region /note= "N-myristoylation site"
FT 181..193 /note= "epidermal growth factor domain cysteine pattern signature"
FT Domain 198..213 /note= "transmembrane domain"
FT Modified-site 205..211 /note= "N-myristoylation site"
XX
FN W0200105972-A1.
XX
PD 25-JAN-2001.
PD 15-MAR-2000; 2000WO-US006884.
PF 20-JUL-1999; 99US-0144758P.
PR (GETH) GENENTECH INC.
PI Ashkenazi AJ, Baker KP, Fong S, Goddard A, Godowski PJ;
PI Gurney AL, Hillan KJ, Mark MR, Marsters SA, Pitti RM, Tumas D;
PI Watanabe CK, Wood WI;
XX WPI; 2001-103149/11.
DR N-PSDB; AAF30054.
XX
PT New PRO polypeptides, nucleic acids and (ant)agonists, useful for
PT diagnosing and treating immune-related disorders, such as multiple
PT sclerosis, rheumatoid arthritis and diabetes.
XX
PS Claim 20; Fig 10; 127pp; English.
CC
CC The present sequence is that of novel human immunomodulator PRO240
CC (UNQ214), as deduced from cDNA (see AAF30054) isolated from a foetal
CC liver library. PRO240 (25 kDa, pI 7.83) shows sequence homology to
CC chicken C-serate-1 and Drosophila serrate precursor protein. Expression
CC was observed in lung cancer, 8 squamous carcinomas and in 6/8
CC adenocarcinomas, in situ and infiltrating components. The invention
CC provides polynucleotides (see AAF30050-62) encoding novel human PRO
CC proteins (see AAB20108-20) including PRO240. Claimed compositions
CC comprising these proteins or their agonists are useful for increasing
CC infiltration of inflammatory cells into a tissue of a mammal, stimulating
CC or enhancing an immune response, or increasing the proliferation of T-
CC lymphocytes in a mammal in response to an antigen. Claimed compositions
CC comprising a PRO polypeptide or its antagonist have the opposite effect.
CC A claimed method for treating an immune related disorder, such as a T
CC cell disorder, involves administering a PRO polypeptide, an agonist
CC antibody or an antagonist antibody. The disorder is selected from
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, spondyloarthropathy, systemic sclerosis,
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, demyelinated diseases (such as multiple sclerosis), autoimmune
CC chronic active hepatitis, primary biliary cirrhosis, granulomatous
CC hepatitis, sclerosing cholangitis, inflammatory bowel disease (ulcerative
CC colitis and Crohn's disease), gluten-sensitive enteropathy, Whipple's
CC disease, (auto)immune-mediated skin diseases (such as bullous skin
CC disease, erythema multiforme and psoriasis), allergic diseases (such as
CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and
CC urticaria), immunologic diseases of the lung and transplantation
CC associated diseases (such as graft rejection and graft-versus-host
CC disease) (all claimed). Claimed methods of diagnosing these disorders
CC comprise detecting the level of expression of the PRO gene. Also claimed
CC are a method of identifying a compound capable of inhibiting the
CC expression or activity of the PRO polypeptide, vectors, host cells,
CC antibodies, and a method of stimulating an immune response in a mammal
CC using PRO240
XX
SQ Sequence 229 AA;

Alignment Scores:
Pred. No.: 4.61e-63 Length: 229

Score: 690.00 Matches: 128
 Percent Similarity: 89.68% Conservative: 11
 Best Local Similarity: 82.58% Mismatches: 16
 Query Match: 77.70% Indels: 1
 DB: 4 Gaps: 0

US-09-773-476-294 (1-489) x AAB20112 (1-229)

QY 3 CTGAGGCTAGATCTTCAGACTGTTCCCT-GAGGATCCTGGTCCAAACTTTTACAGGCT 61
 DB 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
 QY 62 TATACCTGCTATTATCATAGACCTTCAGCAATCCCTCAAGGATGATTGGCCACACCC 121
 DB 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
 QY 122 TTCGCTGGGTTTACTCAGCTGCAGACTCTCATATCTACCAAGATGTTCCCTGCTCGGA 181
 DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132
 QY 182 GGTAGTAATGCTGGGCAATGTTACTTCTTCAAGGACAGCAGATTTCCCAAGGCCAA 241
 DB 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyIleAspAsnGlnIleCysGlnGlyGln 152
 QY 242 AGGACCTTTGCAATAGACTGGAAGCCAGAAATGTCTCAGAACGATCTTGTGCA 301
 DB 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
 QY 302 TCTGACGCTCCTGGTCTTTTGCAGTGGTGTGCTGATGCTTCCATGATACAAAGTGT 361
 DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyIysCys 192
 QY 362 ATGAGGACGGCTCATTTTCACTGCTTATGCTTCTTGGGATTCCTGGATCCACCGCTA 421
 DB 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
 QY 422 GCCATCTNCATTTACTTTGGGAACCCAGCGCCGGAAGCCAAAG 466
 DB 213 SerValSerIleLeuLeuTrpAlaThrGlnArgAlaLys 227

RESULT 9

ID AAB68595 standard; protein; 229 AA.

XX AC AAB68595;

DT 27-APR-2001 (first entry)

XX DE PRO240.

XX KW Cytostatic; PRO protein; tumour; cancer.

XX OS Homo sapiens.

XX BN W0200105836-A1.

XX PD 25-JAN-2001.

XX PF 20-DEC-1999; 99WO-US030999.

XX PR 20-JUL-1999; 99US-0144758P.

XX PR 26-JUL-1999; 99US-0145698P.

XX PR 08-SEP-1999; 99WO-US020594.

XX PR 13-SEP-1999; 99WO-US020944.

XX PR 15-SEP-1999; 99WO-US021090.

XX PR 05-OCT-1999; 99WO-US023089.

XX PR 29-NOV-1999; 99WO-US028214.

XX PR 30-NOV-1999; 99WO-US028313.

XX PR 02-DEC-1999; 99WO-US028564.

XX (GETH) GENENTECH INC.

XX PA Botstein D, Goddard A, Gurney AL, Hillan KJ, Roy MA, Wood WJ;

XX PI

XX WPI; 2001-091968/10.
 DR N-PSDB; AAF60356.

XX PT New antibody that binds to a PRO polypeptide, e.g. PRO187 and PRO533,
 XX useful for diagnosing and treating cancers.

XX PS Claim 61; Fig 8; 196pp; English.

XX CC The present invention relates to PRO proteins and coding sequences. The
 XX present sequence is one such PRO protein. It was found that the PRO genes
 CC are amplified in the genome of tumour cells. The gene amplification is
 CC expected to be associated with the overexpression of the gene product and
 CC contributes to tumorigenesis. Therefore, antagonists of PRO proteins are
 CC useful for the treatment of benign or malignant tumours, leukaemias,
 CC lymphoid malignancies and other disorders such as neuronal, glial,
 CC astrocytal, hypothalamic, glandular, epithelial, inflammatory and
 CC immunologic disorders

XX SQ Sequence 229 AA;

Alignment Scores:

Pred. No.: 4.61e-63 Length: 229
 Score: 690.00 Matches: 128
 Percent Similarity: 89.68% Conservative: 11
 Best Local Similarity: 82.58% Mismatches: 16
 Query Match: 77.70% Indels: 1
 DB: 4 Gaps: 0

US-09-773-476-294 (1-489) x AAB68595 (1-229)

QY 3 CTGAGGCTAGATCTTCAGACTGTTCCCT-GAGGATCCTGGTCCAAACTTTTACAGGCT 61
 DB 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
 QY 62 TATACCTGCTATTATCATAGACCTTCAGCAATCCCTCAAGGATGATTGGCCACACCC 121
 DB 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
 QY 122 TTCGCTGGGTTTACTCAGCTGCAGACTCTCATATCTACCAAGATGTTCCCTGCTCGGA 181
 DB 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132
 QY 182 GGTAGTAATGCTGGGCAATGTTACTTCTTCAAGGACAGCAGATTTCCCAAGGCCAA 241
 DB 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyIleAspAsnGlnIleCysGlnGlyGln 152
 QY 242 AGGACCTTTGCAATAGACTGGAAGCCAGAAATGTCTCAGAACGATCTTGTGCA 301
 DB 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
 QY 302 TCTGACGCTCCTGGTCTTTTGCAGTGGTGTGCTGATGCTTCCATGATACAAAGTGT 361
 DB 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyIysCys 192
 QY 362 ATGAGGACGGCTCATTTTCACTGCTTATGCTTCTTGGGATTCCTGGATCCACCGCTA 421
 DB 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
 QY 422 GCCATCTNCATTTACTTTGGGAACCCAGCGCCGGAAGCCAAAG 466
 DB 213 SerValSerIleLeuLeuTrpAlaThrGlnArgAlaLys 227

RESULT 10

XX AAM51083

ID AAM51083 standard; protein; 229 AA.

XX AC AAM51083;

XX DT 06-JUN-2002 (first entry)

XX DE Human transforming growth factor alpha HIII.

XX XX

KW Transforming growth factor alpha HIII; TGF alpha HIII; human;
 KW antiinflammatory; antitumour; vulnery; ophthalmological;
 KW neuroprotective; antipsoriatic; therapy; diagnosis.

OS Homo sapiens.

PH Key Location/Qualifiers
 FT Peptide 1..25
 FT /label= Signal_peptide
 FT Protein 26..229
 FT /label= Mature_protein
 FT Active-site 126..177
 FT Domain 178..204
 FT /label= Transmembrane_domain

XX US2002025553-A1.

XX 28-FEB-2002.

XX 01-DEC-2000; 2000US-00726349.

XX 04-JAN-1996; 96US-0011136P.

PR 03-JAN-1997; 97US-00778545.

PR 02-DEC-1999; 99US-0169387P.

XX (WEIY/) WEI Y.

XX Wei Y;

XX WPI; 2002-280092/32.

DR N-PSDB; ABA92166.

XX Isolated nucleic acid molecule encoding Transforming Growth Factor alpha
 PT HIII is used in preventing, treating or ameliorating a medical condition
 PT e.g. cardiovascular or autoimmune diseases.

XX Claim 11; Fig 1A-B; 118pp; English.

XX The present sequence is that of human transforming growth factor alpha
 CC HIII (TGF alpha HIII), a novel member of the TGF family. The amino acid
 CC sequence was deduced from a cDNA clone (see ABA92166) discovered in a
 CC human testis cDNA library. The invention provides TGF alpha HIII nucleic
 CC acid molecules and polypeptides (including the mature protein, full-
 CC length secreted protein, variants and homologues), vectors, host cells,
 CC antibodies and recombinant methods for producing the polypeptides. The
 CC TGF alpha HIII polypeptides and polynucleotides can be used in diagnostic
 CC methods for detecting disorders related to TGF alpha HIII, and also for
 CC therapeutic purposes, e.g. to stimulate wound healing to restore normal
 CC neurological functioning after trauma or AIDS dementia, to treat ocular
 CC disorders, to target certain cells, to treat kidney and liver disorders,
 CC to promote hair follicular development, to stimulate angiogenesis for the
 CC treatment of burns, ulcers and corneal incisions, and to stimulate
 CC embryogenesis. Autoimmune diseases, disorders of haematopoietic cells,
 CC allergic reactions, cardiovascular diseases, organ rejection,
 CC inflammation, and hyperproliferative disorders may also be treated.
 CC Methods are also provided for identifying agonists and antagonists of TGF
 CC alpha HIII. Antagonists may be used to inhibit the action of TGF alpha
 CC HIII polypeptides in the treatment of corneal inflammation, neoplasia
 CC such as tumours and cancers, and psoriasis

XX Sequence 229 AA;

Alignment Scores:
 Pred. No.: 4,61e-63 Length: 229
 Score: 690.00 Matches: 128
 Percent Similarity: 89.68% Conservatve: 11
 Best Local Similarity: 82.58% Mismatches: 16
 Query Match: 77.70% Indels: 1
 DB: 5 Gaps: 0

US-09-773-476-294 (1-489) x AAM51083 (1-229)

QY 3 CTGAGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCGTCACAACTTTTACAGGCT 61

Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
 QY 62 TATACTCTATTATCATAGACCTTCAGGCAATCCTCTCAAGGATGATTTGGCCAAACACC 121
 Db 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuGlyGlyAspLeuAlaAsnThr 112
 QY 122 TTCGTGGTTTACTCAGCTGCAGACTCTGATCTACTACCAAGATGTTCCCTGCTCTGGA 181
 Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132
 QY 182 GGTAGTAATGCCTGGGACAATGTACTCTTTCAAGGACAAGCAGATTTGCCAGGGCAA 241
 Db 133 GlyIleAsnAlaIleAsnThrIleThrSerTyrlleAspAsnGlnIleCysGlnGlyGln 152
 QY 242 AGGACCTTTTCAATAGCACTGGAAGCCCAAGAAATGTCTCTGAGAACGGATCTTTGTGCA 301
 Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
 QY 302 TCTGACGCTCTGGTCTTTTTCAGTGGTGTTCGTCGATGTTTCCATGATACAAAGTGT 361
 Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192
 QY 362 ATGAGGCAGGCTCATTTTCACTGCTTATGTTCTTTGGGATTTCTGGATCCACACGCTA 421
 Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
 QY 422 GCCATCTNCAATTTACTTTGGGAAACCCAGCGCGGAAAGCCCAAG 466
 Db 213 SerValSerIleLeuLeuTAlaThrGlnArgArgLysAlaLys 227

RESULT 11

ABG34033
 ID ABG34033 standard; protein; 229 AA.

AC ABG34033;

DT 15-JUL-2002 (first entry)

XX Human Pro peptide #4.

XX Human; PRO; secreted protein; transmembrane protein; genetic disorder;
 KW tumour; cancer.

OS Homo sapiens.

XX WO200224888-A2.

XX 28-MAR-2002.

XX 29-AUG-2001; 2001WO-US027099.

XX 01-SEP-2000; 2000US-0229896P.

XX 05-SEP-2000; 2000US-0230621P.

PR 22-SEP-2000; 2000US-0235147P.

PR 10-NOV-2000; 2000WO-US030873.

PR 12-JAN-2001; 2001US-0261878P.

PR 16-JAN-2001; 2001US-0261910P.

PR 16-JAN-2001; 2001US-0261939P.

PR 16-JAN-2001; 2001US-0262150P.

PR 25-JAN-2001; 2001US-0284395P.

PR 02-FEB-2001; 2001US-0266421P.

PR 09-FEB-2001; 2001US-0267623P.

PR 28-FEB-2001; 2001WO-US006520.

PR 03-MAR-2001; 2001US-0274399P.

PR 03-APR-2001; 2001US-0280982P.

PR 04-APR-2001; 2001US-0282125P.

PR 04-APR-2001; 2001US-0282199P.

PR 25-MAY-2001; 2001US-0290589P.

PR 01-JUN-2001; 2001WO-US017092.

PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.
XX (GETH) GENENTECH INC.
XX Baker KP, Baton DL, Filvaroff E, Goddard A, Grimaldi JC;
PI Gurney AL, Smith V, Stephan J, Watanabe CK, Wood WI, Zhang Z;
PI Fong S;
XX WPI; 2002-362426/39.
DR N-PSDB; ABK69964.
XX
XX New PRO polypeptides and polynucleotides encoding the polypeptides,
PT useful in gene therapy, chromosome identification, tissue typing, or for
PT genetic analysis of individuals with genetic disorders.
XX
XX Claim 11; Fig 8; 218pp; English.
XX
XX This invention relates to the cDNA and protein sequences of novel
CC secreted and transmembrane polypeptides PRO polypeptides. The invention
CC also comprises a method for producing the proteins of the invention by
CC recombinant means and antibodies specific for the protein of the
CC invention. The antibody may be used for detecting the PRO proteins of the
CC invention and may be used to modify their activity. Polynucleotides may
CC be used as hybridisation probes for a cDNA library to isolate the full-
CC length PRO cDNA or to isolate other cDNAs, to construct hybridisation
CC probes for mapping the gene which encodes that PRO and for genetic
CC analysis of individuals with genetic disorders, in assays to identify
CC other proteins or molecules involved in binding reaction, to generate
CC transgenic animals or knock-out animals which in turn are useful in the
CC development and screening of therapeutically useful reagents, for
CC chromosome identification, and tissue typing. The PRO polypeptides are
CC useful in gene therapy, and as molecular weight markers for protein
CC electrophoresis purposes. The sequences may also be used to detect
CC overexpression on PRO polypeptides in cancerous tumours and for screening
CC for differentially expressed genes using microarray technology. The
CC present sequence represents a human PRO protein of the invention
XX
SQ Sequence 229 AA;

Alignment Scores:
Pred. No.: 4,61e-63 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 5 Gaps: 0

US-09-773-476-294 (1-489) x ABG34033 (1-229)
QY 3 CTGAGGCTAGATCTTCAGACTGTCCTC-CAGGATCTGCTGCAACTTTTACAGGCT 61
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnHeHisGlnAla 92

QY 62 TAACTGCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCACAC 121
Db 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112

QY 122 TTCGCTGGGTTCATGAGTCGACACTCTGATCTACTACCAAGATGTCCTGCTCTGGA 181
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132

QY 182 GGTAGTAACTGCTGGGCAATTTACTCTTCTCAAGGACAGCAAGATTTGCCAAGGCCAA 241
Db 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyIleAspAsnGlnIleCysGlnGlyGln 152

QY 242 AGGACCTTTCATAGACATCGAGCCAGCAAGATGTCTGAGAACGGATCTTGTGCA 301
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172

QY 302 TCTGACGCTCTGCTCTTTTGCAGTGGTGTGCTGATGGTTTCCATGATACAAAGTGT 361
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyTyLysCys 192

QY 362 ATGAGCGAGGCTCATTTTCTTCTTATGTTCTTTGGATCTGGGATCCACCAAGCTA 421
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThre 212

QY 422 CCCATCTTCATCTTCTTGGGAAACCCAGCGCCGAAAGCCAAAG 466
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227

RESULT 12
ABU71417
ID ABU71417 standard; protein; 229 AA.
XX
XX AC ABU71417;
XX
XX DT 09-JUN-2003 (first entry)
XX
XX DE Human neoplasia inhibiting PRO polypeptide PRO240.
XX
XX Human; tumour; cancer; neoplasia; liver cancer; sarcoma; breast cancer;
KW ovarian cancer; renal cancer; colorectal cancer; melanoma;
KW uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;
KW gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;
KW central nervous system cancer; hepatic carcinoma; glioblastoma;
KW neuronal disorder; glial disorder; astrocytal disorder;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocellic disorder;
KW inflammatory disorder; angiogenic disorder; immunologic disorder.
XX
XX OS Homo sapiens.
XX
XX PN US2002192209-A1.
XX
XX PD 19-DEC-2002.
XX
XX PF 30-NOV-2001; 2001US-00001054.
XX
XX PR 17-SEP-1997; 97US-0059114P.
PR 27-MAR-1998; 98US-0079689P.
PR 30-MAR-1998; 98US-0079920P.
PR 24-APR-1998; 98US-0082999P.
PR 29-APR-1998; 98US-0083545P.
PR 12-MAY-1998; 98US-0085149P.
PR 02-JUN-1998; 98US-0087607P.
PR 11-JUN-1998; 98US-0088589P.
PR 25-JUN-1998; 98US-0090691P.
PR 17-AUG-1998; 98US-0096891P.
PR 17-AUG-1998; 98US-0096894P.
PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100263P.
PR 15-SEP-1998; 98US-0100390P.
PR 23-SEP-1998; 98US-0101476P.
PR 18-NOV-1998; 98US-0107783P.
PR 19-NOV-1998; 98US-0108849P.
PR 15-DEC-1998; 98US-0112420P.
PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.
PR 12-JAN-1999; 99US-0115554P.
PR 12-JAN-1999; 99US-0115558P.
PR 20-JAN-1999; 99US-0116533P.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-APR-1999; 99US-00284291.
PR 20-APR-1999; 99WO-US008615.
PR 27-APR-1999; 99US-0131294P.
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.

PR	01-SEP-1999;	99WO-US020111.
PR	08-SEP-1999;	99WO-US020594.
PR	09-SEP-1999;	99US-00380913.
PR	18-OCT-1999;	99US-00403297.
PR	29-OCT-1999;	99US-0162506P.
PR	10-NOV-1999;	99US-00423741.
PR	30-NOV-1999;	99WO-US028313.
PR	01-DEC-1999;	99WO-US028634.
PR	02-DEC-1999;	99WO-US028551.
PR	09-DEC-1999;	99US-0170262P.
PR	16-DEC-1999;	99WO-US030095.
PR	20-DEC-1999;	99WO-US030999.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US003565.
PR	18-FEB-2000;	2000WO-US004341.
PR	18-FEB-2000;	2000WO-US004342.
PR	02-MAR-2000;	2000WO-US005841.
PR	03-MAR-2000;	2000US-0187202P.
PR	15-MAR-2000;	2000WO-US006884.
PR	30-MAR-2000;	2000WO-US008439.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014042.
PR	30-MAY-2000;	2000WO-US014941.
PR	02-JUN-2000;	2000WO-US015264.
PR	11-AUG-2000;	2000WO-US022031.
PR	23-AUG-2000;	2000WO-US023522.
PR	08-NOV-2000;	2000US-00709238.
PR	10-NOV-2000;	2000WO-US030873.
PR	01-DEC-2000;	2000WO-US032678.
PR	28-FEB-2001;	2001WO-US006520.
PR	01-MAR-2001;	2001WO-US006666.
PR	09-MAR-2001;	2001US-00802706.
PR	25-MAY-2001;	2001US-00866034.
PR	25-MAY-2001;	2001WO-US017092.
PR	01-JUN-2001;	2001US-00872034.
PR	01-JUN-2001;	2001US-00872035.
PR	01-JUN-2001;	2001WO-US017800.
PR	14-JUN-2001;	2001US-00982636.
PR	20-JUN-2001;	2001WO-US019692.
PR	29-JUN-2001;	2001WO-US021066.
PR	09-JUL-2001;	2001WO-US021735.
PR	30-JUL-2001;	2001US-00918585.
PR	06-AUG-2001;	2001US-00924419.
PR	09-AUG-2001;	2001US-00927796.
PR	13-AUG-2001;	2001US-00929404.
PR	28-AUG-2001;	2001US-00941992.
PR	29-AUG-2001;	2001WO-US027099.
PR	04-SEP-2001;	2001US-00946374.
XX	(GETH) GENENTECH INC.	PA

XX	Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI	Shelton DL, Smith V, Watanabe CK, Wood WI;
XX	WPI; 2003-328851/06.
DR	N-PSDB; ACA57990.
XX	
PT	Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
PT	treating tumor, preferably cancer, or for treating neuronal, glial,
PT	hypothalamic, stromal, inflammatory, angiogenic and immunologic
PT	disorders.
PT	

XX PS Claim 32; Fig 2; 186pp; English.

The invention relates to an isolated secreted and transmembrane polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its associated signal peptide or PRO polypeptide extracellular domain with or without its associated signal peptide. The PRO polypeptide or an antibody binding to it is useful for inhibiting the growth of a tumor cell. A composition containing a PRO polypeptide is useful for inhibiting neoplastic cell growth or for treating a tumour, preferably cancer (such as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder, gastric, pancreatic, vulval, thyroid, central nervous system

carcin, hepatic carcinomas, sarcomas, glioblastomas, melanoma or leukaemia) in a mammal. The PRO polypeptide is useful for identifying its agonists. The PRO polypeptide or an antibody binding to it is useful in the preparation of a medicament for treating a condition which is responsive to the PRO polypeptide or an antibody binding to it. The PRO polypeptide or an antibody binding to it is also useful for treating neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, epithelial, stromal, blastocoelic, inflammatory, angiogenic and immunologic disorders. The present sequence represents the amino acid sequence of a PRO polypeptide of the invention

Sequence 229 AA;

Alignment Scores:

4.61e-63	Length:	229
Pred. No.:	Matches:	128
Score:	Percent Similarity:	89.66%
Score:	Conservative:	11
Best Local Similarity:	Mismatches:	16
Best Local Similarity:	Indels:	1
Query Match:	Gaps:	0
DB:		

US-09-773-476-294 (1-489) x ABU71417 (1-229)

3	CTGAGGTAGATCTTCAGAACTGTTCCCT - GAGGATCTGTGTCCTCAAACTCTTTTACAGGCT	61
73	LeuglyLeuAspLeuGlnAenCysSerLeuGluAAspProGlyProAsnPheHisGlnAla	92
62	TATACTGCTATTATCATAGACCTTCAGGCAAAATCCTCTCAAGGATGANTTTGGCCAAACACC	121
93	HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr	112
122	TTCCGTGGGTTTTACTCAGCTGCGAGACTCTGATACTACCACAAGATGTTCCCTGTCTCTCGGA	181
113	PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly	132
192	GGTAGTAATGCTGGGACAATGTTACTTCTTCAAGGACAACGAGATTTGCCAAGGGCAA	241
133	GlyIleAsnAlaTrpAsnThrIleThrSerTrileAspAsnGlnIleCysGlnGlyGln	152
242	AGGAGACCTTTGCAATACACTGCAAGCCAGCAAAATGTGTCCTGAGAACGGATCTTGTGTGCA	301
153	LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal	172
302	TCTGACGCTGCTGCTCTTTTGCAGTCGGTWTGTGTGATGGTTTCATGGATACAAAGTGT	361
173	ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTrpLysCys	192
362	ATGAGGACGGGCTCATTTTCACCTGCTATGTCTCTTTGGGATCTGGGATCCACCAAGCTTA	421
193	MetArgGlnGlySerPheSerLeuLeuMetPheGlyIleLeuGlyAlaIleThrThrLeu	212
422	GCCATCTNCATCTTACTTTGGGAAACCCAGCGCCGGAAAGCCCAAG	466
213	SerValSerIleLeuLeuTroAlaThrGlnArgAlaLysAlaLys	227

RESULT 13

ADA01276

ID	ADA01276	standard; protein; 229 AA.
1	1	1
2	2	2
3	3	3
4	4	4
5	5	5
6	6	6
7	7	7
8	8	8
9	9	9
10	10	10
11	11	11
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16	16	16
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95	95	95
96	96	96
97	97	97
98	98	98
99	99	99
100	100	100

XX

AC ADA01276;



DT 06-NOV-2003 (first entry)

THE

Human PRO polypeptide #4.

XX

Human; PFG; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor- α ; TNF- α ; blood; chondrocyte cell; tumour; adrenal; lung; colon; breast; prostate; rectum; cervix; liver; cancer; microvascular endothelial cell; endothelial cell tube formation; sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthritis; osteopathic; antirheumatic; antiarthritic.

[illegible]

OS Homo sapiens.

XX US2003068779-A1.
 XX 10-APR-2003.
 XX 16-SEP-2002; 2002US-00245107.
 XX 09-MAY-2001; 2001US-0290589P.
 XX 29-AUG-2001; 2001WO-US027099.
 XX 18-JUL-2002; 2002US-00197942.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 XX Fong S;
 XX WPI; 2003-625484/59.
 XX N-PSDB; ADA01275.
 XX Novel isolated PRO1313, PRO20080 or PRO21383 polypeptide useful for
 XX stimulating proliferation of human microvascular endothelial cells, and
 XX PRO6018 polypeptide useful for stimulating proliferation of chondrocyte
 XX cells.
 XX Claim 11; Fig 8; 307pp; English.
 XX The invention relates to isolated human PRO polypeptides (secreted and
 XX transmembrane polypeptides) and the polynucleotides encoding them. The
 XX invention also relates to an antibody which specifically binds to a PRO
 XX polypeptide, a method for stimulating the release of tumour necrosis
 XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the
 XX proliferation or differentiation of chondrocyte cells and a method for
 XX detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
 XX colon, breast, prostate, rectal, cervical and liver tumours). The
 XX polynucleotides are useful in molecular biology, including uses as
 XX hybridisation probes, in chromosome and gene mapping, in generating
 XX antisense RNA and DNA and in gene therapy. The polynucleotides may also
 XX be used in preparing PRO polypeptides by recombinant techniques and in
 XX generating either transgenic animals or knock-out animals which are
 XX useful in the development and screening of therapeutically useful
 XX reagents. The PRO polypeptides or antibodies are used in preparing a
 XX medicament for treating a condition responsive to the polypeptides or
 XX antibodies, such as tumours, for stimulating and inhibiting proliferation
 XX of human microvascular endothelial cells, for inducing endothelial cell
 XX tube formation and for treating sports-related joint problems, articular
 XX cartilage defects, osteoarthritis and rheumatoid arthritis. This sequence
 XX represents a human PRO polypeptide of the invention.
 XX
 SQ Sequence 229 AA;
 Alignment Scores:
 Pred. No.: 4.61e-63 Length: 229
 Score: 690.00 Matches: 128
 Percent Similarity: 89.68% Conservative: 11
 Best Local Similarity: 82.58% Mismatches: 16
 Query Match: 77.70% Indels: 1
 DB: 6 Gaps: 0
 US-09-773-476-294 (1-489) x ADA01276 (1-229)
 QY 3 CTGAGGCTAGACTCTCAGAACTGTCCTTCCCT-GAGGATCTGGTCCAACTTTTACAGGCT 61
 Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnHisGlnAla 92
 QY 62 TATACGTCTATTATCATAGACTCTCAGGAAATCTCTCAAGATGATTTGCCAACACC 121
 Db 93 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuGlyAspLeuAlaAsnThr 112
 QY 122 TTCCTGGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGCTCGA 181
 Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132

QY 182 GGTAGTAATGCTGGGACAATGTTACTTCTTCAAGGACAAGCAGATTGCGCAAGGGCAA 241
 Db 133 GlyIleAsnAlaIleAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln 152
 QY 242 AGGACACCTTTGCAATAGACACTGGAGAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCA 301
 Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
 QY 302 TCTGACGCTCTGCTCTTTTTCAGTGGCTTGTCTGCTGATGGTTTCCATGGATACAAAGTGT 361
 Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192
 QY 362 ATGAGGACAGGCTCATTTTTCATCTGCTTATGTTCTTGGGATTTCTGGATCCACACGCTA 421
 Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
 QY 422 GCCATCTTNCATCTTACTTGTGGGAAACCCAGCGCCGGAAGCCAAAG 466
 Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227
 RESULT 14
 ADA43705
 ID ADA43705 standard; protein; 229 AA.
 XX AC ADA43705;
 XX DT 20-NOV-2003 (first entry)
 XX DE Human secreted/transmembrane polypeptide PRO240.
 XX Human; PRO; secreted protein; transmembrane protein;
 XX endothelial cell tube formation; chondrocyte cell differentiation;
 XX microvascular endothelial cell; tumour; lung tumour; colon tumour;
 XX breast tumour; prostate tumour; rectal tumour; kidney tumour;
 XX liver tumour; cytostatic; vaccine.
 XX Homo sapiens.
 XX US2003064474-A1.
 PD 03-APR-2003.
 PF 16-SEP-2002; 2002US-00245859.
 XX 29-AUG-2001; 2001WO-US027099.
 PR 18-JUL-2002; 2002US-00197942.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Eaton DL, Filvaroff E, Goddard A, Grimaldi JC;
 XX Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI, Zhang Z;
 XX Fong S;
 XX WPI; 2003-605867/57.
 XX N-PSDB; ADA43704.
 XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO20080 or
 XX PRO21383, useful in molecular biology, chromosome and gene mapping, in
 XX generating antisense RNA and DNA, and in gene therapy.
 XX Claim 11; Fig 8; 308pp; English.
 XX The invention relates to an isolated secreted/transmembrane (PRO)
 XX polypeptide, having at least 80% sequence identity to a sequence selected
 XX from any one of the 57 amino acid sequences given in specification, or to
 XX a sequence encoded by a nucleic acid molecule selected from any one of
 XX the nucleic acids deposited under any of the ATCC accession numbers given
 XX in specification, or a sequence having at least 80% identity to PRO
 XX lacking its associated signal peptide, an extracellular domain of PRO
 XX with or without its associated signal peptide. Also included are vectors,
 XX transformed host cells, anti-PRO antibodies, the nucleic acids encoding
 XX PRO, PRO fusion proteins, inducing endothelial cell tube formation (by
 XX administering PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000,

QY	3	CTGAGCGTAGATCTTCACAACTGTTCCCT--CAGATCCTCGTCCCAACTTTTTACAGCGT	61
Db	73	LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla	92
QY	62	TATACTGCTATTATCATAGACTTCAGGCAAACTCCTCAAGGATGATTGGCCAAACACC	121
Db	93	HisThrThrValIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr	112
QY	122	TTCCGTGGGTTTACTCAGCTCGAGACTCTGATCTACTACCAAGAATGTTCCCTGTCCTGGA	181
Db	113	PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnCysProGly	132
QY	182	GGTAGTAAATGCTGGGACAAGTTTACTTCTTCAAGGACAAAGCAGAGATTTGCCAAGGGCAA	241
Db	133	GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln	152
QY	242	AGGACCTTTGCAATAGCACTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCA	301
Db	153	LysAsnLeuCysAsnAsnThrGlyAspProGlnMetCysProGluAsnGlySerCysVal	172
QY	302	TCTGACGTCCTGGTCTTTTCAGTCGGTTTGTCTGCTCATGGTTCCATGATACAGTCT	361
Db	173	ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys	192
QY	362	ATGAGCAGCGGCTCATTTTTCATGCTTATGTTCTTTGGGATCTGGGATCCACACGCTTA	421
Db	193	MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyLeuGlyAlaThrThrLeu	212
QY	422	GCATCTNCAATCTACTTTGGGGAAACCCAGCGCCGGAAAGCCCAAG	466
Db	213	SerValSerIleLeuLeuTrpAlaThrGlnArgGlyAlaLys	227

The invention relates to an isolated secreted/transmembrane (PRO) polypeptide, having at least 80% sequence identity to a sequence selected from any one of the 57 amino acid sequences given in specification, or to a sequence encoded by a nucleic acid molecule selected from any one of the nucleic acids deposited under any of the ATCC accession numbers given in specification, or a sequence having at least 80% identity to PRO lacking its associated signal peptide, an extracellular domain of PRO with or without its associated signal peptide. Also included are vectors, transformed host cells, anti-PRO antibodies, the nucleic acids encoding PRO, PRO fusion proteins, inducing endothelial cell tube formation (by administering PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 or PRO34274 polypeptide or its agonist) and an oligonucleotide probe derived from any one of the above nucleotide sequences. PRO6018 polypeptide is useful for stimulating the proliferation or differentiation of chondrocyte cells. PRO1313, PRO20080 and PRO21383 polypeptides are useful for stimulating the proliferation of human microvascular endothelial cells. PRO6071, PRO4487 and PRO6006 polypeptides are useful for inhibiting the proliferation of human microvascular endothelial cells. PRO polypeptides are useful for detecting the presence of tumour in a mammal including tumours of lung, colon, breast, prostate, rectal, kidney and liver. PRO281, PRO1560, PRO189, PRO499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 and PRO34274 polypeptides are useful for inducing endothelial cell tube formation. PRO or the antibody are useful in the preparation of a medicament for treating a condition responsive to PRO polypeptide. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences, for measuring or detecting the expression of an associated gene, and as antisense probes. PRO nucleic acid is useful as a hybridisation probe in chromosome and gene mapping, in the generation of antisense RNA and DNA, and for the preparation PRO polypeptides. PRO and PRO nucleic acid are useful as therapeutic agents, e.g. vaccines. The present sequence represents a PRO protein.

Sequence 229 AA;

Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 6 Gaps: 0

US-09-773-476-294 (1-489) x ADA43473 (1-229)

Qy	3	CTGAGGCTAGACTCTCAGACTGTTCCCT-GAGATCCTGGTCCAAACTTTTACAGGCT	61
Db	73	LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla	92
Qy	62	TATACTGCTATTATCATAGACCTTCAGGCAATCCTCTCAAGGATGATTTGGCCAAACACC	121
Db	93	HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr	112
Qy	122	TTCCGTGGGTTTACTCAGCTCCAGACTCTCATACTACCAAGATGTTCCCTCTCCTGGA	181
Db	113	PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly	132
Qy	182	GGTAGTAATGCTGGGCAATGTTACTTCTTCAAGGACAAGCAGATTTGCCAAGGGCAA	241
Db	133	GlyIleAsnAlaIleAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln	152
Qy	242	AGGACCTTTTGCAATAGACTGGAAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCA	301
Db	153	LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal	172
Qy	302	TCTGACGGTCTGCTCTTTTGCAGTGGTGTGTGCTGATGCTTCCATGGATACAAAGTGT	361
Db	173	ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys	192
Qy	362	ATGAGGCAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATTTCTGGATCCACCGCTA	421
Db	193	MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu	212
Qy	422	GCCATCTNCATTTCTATTGGGAAACCCAGCGCGGAAAGCCAAAG	466
Db	213	SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys	227

Search completed: June 25, 2004, 09:13:51
Job time : 58 secs

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 25, 2004, 09:11:53 ; Search time 17 Seconds
(without alignments)
5533.842 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 888

Sequence: 1 gactgagctagattcttag.....tnatgagccacacaagactt 489

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 566732

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-O=/cpn2_1/USPTO_spool_p/US09773476/runat_25062004_090847_5839/app_query.fasta_1.647
-DB=PR78 -QFM=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09773476 @CNC 1 1 38 @runat_25062004_090847_5839 -NCPU=3
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR 78:*

- 1: pir1:*
- 2: pir2:*
- 3: pir3:*
- 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	12.7	1203	A49175	Notch B protein -
2	112	12.6	2471	A49128	cell-fate determin
3	103	11.6	2318	S45306	notch 3 protein -
4	103	11.6	2531	A46019	notch-1 protein -
5	102	11.5	2703	A24420	notch protein - fr
6	100.5	11.3	308	JC7125	epidermal growth f
7	100.5	11.3	1722	E89753	protein FilC7.4 (i
8	99	11.1	2809	T30213	G-cadherin - sea u
9	98.5	11.1	1712	A38261	masking protein pr
10	98.5	11.1	2311	S78549	notch3 protein - h
11	98	11.0	2531	S18188	notch protein homo
12	97.5	11.0	1964	T09059	notch4 - mouse
13	95.5	10.8	385	A54785	preadipocyte facto
14	95.5	10.8	1394	A35626	transforming growt

15	95	10.7	616	2	T29234	hypothetical prote
16	95	10.7	675	1	KXRTS	plasma protein S p
17	95	10.7	4391	2	A38096	perlecan precursor
18	94.5	10.6	1220	2	A56136	jagged protein pre
19	94.5	10.6	2437	2	S42612	transmembrane prot
20	94	10.6	383	2	S53716	delta-like homeoti
21	94	10.6	2352	2	T30201	Notch homolog prot
22	93.5	10.5	2531	2	T31070	notch homolog - se
23	93.5	10.5	2555	2	A40043	notch protein homo
24	92.5	10.4	2524	2	A35844	notch protein - Af
25	92.5	10.4	2907	2	A57278	fibrillin-2 precur
26	92.5	10.4	2918	2	A54105	fibrillin-2 precur
27	92.5	10.4	4544	1	S02392	alpha-2-macroglobu
28	92	10.4	861	2	A48825	Notch homolog Motc
29	91	10.2	1408	2	S16148	gene serrate prote
30	90.5	10.2	642	2	S53433	plasma protein S p
31	90.5	10.2	4545	1	S25111	alpha-2-macroglobu
32	89.5	10.1	473	2	A56175	adhesive plaque pr
33	89.5	10.1	1820	2	A55494	latent transformin
34	89	10.0	1064	2	A40136	fibropellin Ia - s
35	88.5	10.0	385	2	S53718	homeotic protein d
36	88.5	10.0	685	2	S78040	fibulin, splice fo
37	88.5	10.0	705	2	S34968	fibulin, splice fo
38	88	9.9	2531	2	T16743	hypothetical prote
39	87.5	9.9	1620	2	T27283	hypothetical prote
40	87	9.8	2180	2	T29764	hypothetical prote
41	87	9.8	2871	2	A55567	fibrillin I - bovi
42	87	9.8	2871	2	A55624	fibrillin-1 precur
43	87	9.8	3002	2	A47221	fibrillin 1 precur
44	86	9.7	259	2	T21011	hypothetical prote
45	86	9.7	1469	2	B36665	slit protein 2 pre

ALIGNMENTS

RESULT 1

A49175
Notch B protein - mouse (fragment)
N:Alternate names: Notch homolog
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence revision 05-Jan-1996 #text_change 08-Sep-2002
C:Accession: A49175; PH1570; S32113
R:Lardelli, M., Lendahl, U.
Exp. Cell Res. 204, 364-372, 1993
A:Title: Notch A and Notch B--two mouse Notch homologues coexpressed in a wide variety of
A:Reference number: A49175; MUID:93178563; PMID:8440332
A:Accession: A49175
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1203 <LAR>
A:Cross-references: EMBL:X68279; NID:g287989; PIDN:CAA48340.1; PID:g287990
A:Experimental source: embryo
A>Note: sequence extracted from NCBI backbone (NCBIP:126158)
C:Comment: This protein has many EGF repeats and lin-12/Notch repeats.
C:Comment: This protein is one of the neurogenic proteins controlling the decision betwee
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:143-174/Domain: EGF homology <EGX1>
F:482-513/Domain: EGF homology <EGF1>
F:560-591/Domain: EGF homology <EGF>
F:674-705/Domain: EGF homology <EGX2>
F:712-743/Domain: EGF homology <EGF3>
F:836-867/Domain: EGF homology <EGX3>

Alignment Scores:

Pred. No.: 0.00524 Length: 1203
Score: 113.00 Matches: 38
Percent Similarity: 33.58% Conservative: 7
Best Local Similarity: 28.36% Mismatches: 36
Query Match: 12.73% Indels: 53
DB: 2 Gaps: 6

US-09-773-476-294 (1-489) x A49175 (1-1203)

QY 98 CTCAGAGATGATTTGGCCACACCTTCCGTGGGTTTACTCAGCTGCAGACTCTGATACTA 157
Db 595 IleAsnAspCysLeuAlaAsn----- 601
QY 158 CCACAAGATGTTCCCTGCTGAGGTAGTAATCCCTGGGACAAATGTTACTTCTTTCAAG 217
Db 602 -----ProCysGlnAsnGlySerCysValAspHisValAsnThrPheSer 617
QY 218 -----GACAAGCAGATTTGCCAAGGGCAAGGGACCTT 250
Db 618 CysGlnCysHisProGlyPheIleGlyAspLys-----CysGlnThrAspMetAsnGlu 635
QY 251 TGCATAGCACTGGAAGCCAGAAATGTCTCTGAGAACGGATCTGTGTCATCTGACGGT 310
Db 636 CysLeuSer-----GluProCysLysAsnGlyGlyThrCys---SerAspTyr 650
QY 311 CCTGGTCTTTTGCAGTGGTGTGCTGATGTTTCCATGATACAAAGTGTATGAGCGAG 370
Db 651 ValAsnSerTyrThrCysThrCysProAlaGlyPheHisGlyValHisCysGluAsnAsn 670
QY 371 -----GGC 373
Db 671 IleAspGluCysThrGluSerSerCysPheAsnGlyGlyThrCysValAspGlyIleAsn 690
QY 374 TCATTTTCACTGCTTATGTTCTTTGGGATTTCTGGATCCA 413
Db 691 SerPheSer-CysLeuCysProValGlyPheThrGlyPro 703
RESULT 2
cell-fate determining gene Notch2 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 02-Aug-2002
C:Accession: A49128
F:Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 116, 931-941, 1992
A:Title: Notch2: a second mammalian Notch gene.
A:Reference number: A49128; MUID:93202015; PMID:1295745
A:Accession: A49128
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-2471 <WEI>
A:Experimental source: Schwann cell
A:Note: sequence extracted from NCBI backbone (NCBIP:127811)
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:264-295/Domain: EGF homology <EGX1>
F:799-830/Domain: EGF homology <EGF1>
F:877-908/Domain: EGF homology <EGX2>
F:1029-1060/Domain: EGF homology <EGF>
F:1067-1098/Domain: EGF homology <EGX3>
F:1153-1184/Domain: EGF homology <EGF3>
F:1191-1222/Domain: EGF homology <EGX4>
F:1876-1908/Domain: ankyrin repeat homology <AN1>
F:1809-1941/Domain: ankyrin repeat homology <AN2>
F:1943-1975/Domain: ankyrin repeat homology <AN3>
F:1976-2008/Domain: ankyrin repeat homology <AN4>
F:2009-2041/Domain: ankyrin repeat homology <AN5>

Alignment Scores:
Pred. No.: 0.00628 Length: 2471
Score: 112.00 Matches: 38
Percent Similarity: 32.84% Conservative: 6
Best Local Similarity: 28.36% Mismatches: 37
Query Match: 12.61% Indels: 53
DB: 2 Gaps: 6

US-09-773-476-294 (1-489) x A49128 (1-2471)

QY 98 CTCAGAGATGATTTGGCCACACCTTCCGTGGGTTTACTCAGCTGCAGACTCTGATACTA 157
Db 912 IleAsnAspCysLeuAlaAsn----- 918
QY 158 CCACAAGATGTTCCCTGCTGAGGTAGTAATCCCTGGGACAAATGTTACTTCTTTCAAG 217

Db 919 -----ProCysGlnAsnGlySerCysValAspLysValAsnThrPheSer 934
QY 218 -----GACAAGCAGATTTGCCAAGGGCAAGGGACCTT 250
Db 935 CysLeuCysLeuProGlyPheValGlyAspLys-----CysGlnThrAspMetAsnGlu 952
QY 251 TGCATAGCACTGGAAGCCAGAAATGTCTCTGAGAACGGATCTGTGTCATCTGACGGT 310
Db 953 CysLeuSer-----GluProCysLysAsnGlyGlyThrCys---SerAspTyr 967
QY 311 CCTGGTCTTTTGCAGTGGTGTGCTGATGTTTCCATGATACAAAGTGTATGAGCGAG 370
Db 968 ValAsnSerTyrThrCysThrCysProAlaGlyPheHisGlyValHisCysGluAsnAsn 987
QY 371 -----GGC 373
Db 988 IleAspGluCysThrGluSerSerCysPheAsnGlyGlyThrCysValAspGlyIleAsn 1007
QY 374 TCATTTTCACTGCTTATGTTCTTTGGGATTTCTGGATCCA 413
Db 1008 SerPheSer-CysLeuCysProValGlyPheThrGlyPro 1020
RESULT 3
S45306
notch 3 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 02-Aug-2002
C:Accession: S45306
R:Lardelli, M.; Dahlstrand, J.; Lendahl, U.
Mech. Dev. 146, 123-136, 1994
A:Title: The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-1
A:Reference number: S45306; MUID:95001556; PMID:7918097
A:Accession: S45306
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2318 <LAR>
A:Cross-references: EMBL:X74760; NID:9483580; PID:CAAS22776.1; PID:9483581
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:163-195/Domain: EGF homology <EGF1>
F:474-505/Domain: EGF homology <EGF2>
F:1839-1871/Domain: ankyrin repeat homology <AN1>
F:1872-1904/Domain: ankyrin repeat homology <AN2>
F:1906-1938/Domain: ankyrin repeat homology <AN3>
F:1939-1971/Domain: ankyrin repeat homology <AN4>
F:1972-2004/Domain: ankyrin repeat homology <AN5>
Alignment Scores:
Pred. No.: 0.0488 Length: 2318
Score: 103.00 Matches: 28
Percent Similarity: 40.62% Conservative: 11
Best Local Similarity: 29.17% Mismatches: 21
Query Match: 11.60% Indels: 36
DB: 2 Gaps: 5
US-09-773-476-294 (1-489) x S45306 (1-2318)

QY 140 CTGCAGACTCTGATACACCAAGATGTTCCCTGT----- 175
Db 689 LeuProLeuCysLeuProAlaAsnHisProCysAlaHisLysProCysSerHisGly 708
QY 176 -----CCTGGAGGTAGTAATCCCTGGGACAAATGTTACTTCTTTCAAGGAC 220
Db 709 ValCysHisAspAlaProGlyPheArgCys----- 719
QY 221 AAGCAGATTTGCCAA-----GGCCAAAGGGACCTTTTGCATAGCACTGGAAGC 268
Db 720 -----ValCysGluProGlyTyrSerGlyProArg-----CysSerGlnSerLeuAla 735
QY 269 CCAGAAATGTCTCTCTAG-----AACGATCTTGTGTCATCTGACGGTCT 313
Db 736 ProAspAlaCysGluSerGlnProCysGlnAlaGlyThrCysThrSerAspGlyLeu 755

A:Residues: 1-2703 <XID>
A:Cross-references: GB:K03508; NID:9157991; PIDN:AAA28725.1; PID:gl57993
R:Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
Cell 43, 567-581, 1985
A:Reference number: A24768; MUID:86079539; PMID:3935325
A:Accession: A24768
A:Molecule type: mRNA
A:Residues: 1-48, 'I', 50-118, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958, 'R', 960-1000, 'I', 1002-1003, 'R', 1005-1006, 'I', 1008-1009, 'R', 1011-1012, 'I', 1014-1015, 'R', 1017-1018, 'I', 1020-1021, 'R', 1023-1024, 'I', 1026-1027, 'R', 1029-1030, 'I', 1032-1033, 'R', 1035-1036, 'I', 1038-1039, 'R', 1041-1042, 'I', 1044-1045, 'R', 1047-1048, 'I', 1050-1051, 'R', 1053-1054, 'I', 1056-1057, 'R', 1059-1060, 'I', 1062-1063, 'R', 1065-1066, 'I', 1068-1069, 'R', 1071-1072, 'I', 1074-1075, 'R', 1077-1078, 'I', 1080-1081, 'R', 1083-1084, 'I', 1086-1087, 'R', 1089-1090, 'I', 1092-1093, 'R', 1095-1096, 'I', 1098-1099, 'R', 1101-1102, 'I', 1104-1105, 'R', 1107-1108, 'I', 1110-1111, 'R', 1113-1114, 'I', 1116-1117, 'R', 1119-1120, 'I', 1122-1123, 'R', 1125-1126, 'I', 1128-1129, 'R', 1131-1132, 'I', 1134-1135, 'R', 1137-1138, 'I', 1140-1141, 'R', 1143-1144, 'I', 1146-1147, 'R', 1149-1150, 'I', 1152-1153, 'R', 1155-1156, 'I', 1158-1159, 'R', 1161-1162, 'I', 1164-1165, 'R', 1167-1168, 'I', 1170-1171, 'R', 1173-1174, 'I', 1176-1177, 'R', 1179-1180, 'I', 1182-1183, 'R', 1185-1186, 'I', 1188-1189, 'R', 1191-1192, 'I', 1194-1195, 'R', 1197-1198, 'I', 1200-1201, 'R', 1203-1204, 'I', 1206-1207, 'R', 1209-1210, 'I', 1212-1213, 'R', 1215-1216, 'I', 1218-1219, 'R', 1221-1222, 'I', 1224-1225, 'R', 1227-1228, 'I', 1230-1231, 'R', 1233-1234, 'I', 1236-1237, 'R', 1239-1240, 'I', 1242-1243, 'R', 1245-1246, 'I', 1248-1249, 'R', 1251-1252, 'I', 1254-1255, 'R', 1257-1258, 'I', 1260-1261, 'R', 1263-1264, 'I', 1266-1267, 'R', 1269-1270, 'I', 1272-1273, 'R', 1275-1276, 'I', 1278-1279, 'R', 1281-1282, 'I', 1284-1285, 'R', 1287-1288, 'I', 1290-1291, 'R', 1293-1294, 'I', 1296-1297, 'R', 1299-1300, 'I', 1302-1303, 'R', 1305-1306, 'I', 1308-1309, 'R', 1311-1312, 'I', 1314-1315, 'R', 1317-1318, 'I', 1320-1321, 'R', 1323-1324, 'I', 1326-1327, 'R', 1329-1330, 'I', 1332-1333, 'R', 1335-1336, 'I', 1338-1339, 'R', 1341-1342, 'I', 1344-1345, 'R', 1347-1348, 'I', 1350-1351, 'R', 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Proc. Natl. Acad. Sci. U.S.A. 87, 8835-8839, 1990			
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Nature 383, 707-710, 1996
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A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 67-113;138-194;268-333; 'G', 335-346;536-613;716-765;1240-1279;1815-1888 <JOU2>
A:Cross-references: EMBL:U97669
C:Genetics:
A:Gene: notch3
A:Map position: 19p13.1
C:Function:
A:Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and C/Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: tandem repeat; transmembrane protein
F:123-155/Domain: EGF homology <EGX1>
F:162-194/Domain: EGF homology <EGF1>
F:240-271/Domain: EGF homology <EGX2>
F:318-349/Domain: EGF homology <EGF>
F:473-504/Domain: EGF homology <EGX3>
F:853-884/Domain: EGF homology <EGF3>
F:928-959/Domain: EGF homology <EGX4>
F:1838-1870/Domain: ankyrin repeat homology <AN1>
F:1871-1903/Domain: ankyrin repeat homology <AN2>
F:1905-1937/Domain: ankyrin repeat homology <AN3>
F:1938-1970/Domain: ankyrin repeat homology <AN4>
F:1971-2003/Domain: ankyrin repeat homology <AN5>
Alignment Scores:
Pred. No.: 0.136 Length: 2321
Score: 98.50 Matches: 39
Percent Similarity: 30.56
Best Local Similarity: 27.08% Mismatches: 45
Query Match: 11.09% Indels: 55
DB: 2 Gaps: 5
US-09-773-476-294 (1-489) x S78549 (1-2321)
QY 52 TTTACAGCCTTACTGCTATTATCATAGCTTCAGGCAATCTCTCAAGGATGATT 111
Db 461 PheThrGlyThrTyCys----- 466
QY 112 GGCCACACCTTCGGGGTTACTCAGTCGACACTGATACCTACCCACAGATGTTCC 171
Db 467 -----GluValAspIleAspGluCys-GlnSerSerPr 477
QY 172 CTGTCCTGGAGGTAGTAATCCCTGGGCAATGTTACTTCTTCAAG----- 217
Db 477 OCysValAsnGlyValCysIleAspArgValAsnGlyPheSerCysThrCysProSe 497
QY 218 -----GACACAGAGATTTGCCAAGGGCAAGGGACCTTTGCAATAGCACTGGAAGCCC 270

Db 497 rGlyPheSerGlySerThrCysGlnLeuAspValAspGluCysAlaSerThr----- 514
QY 271 AGAAATGTCTCTGAGAACGGATCTTGTGCATCTGCAGGTCCTGCTCTTTTGCAGTGGT 330
Db 515 ----ProCys---ArgAsnGlyAlaLysCysValAspGlnProAspGlyTyGluCysAr 532
QY 331 TTGTCCTGATGGTTTCCATGATACAGTGTATAGGCAG----- 370
Db 532 gCysAlaGluGlyPheGluGlyThrLeuCysAspArgAsnValAspCysSerProAs 552
QY 371 -----GGCTCATTTTCACTGCTTATGTTCTT 396
Db 552 pProCysHisHisGlyArgCysValAspGlyIleAlaSerPheSer-CysAlaCysAlap 572
QY 397 TGGGATTC 404
Db 572 roGlyTy 574
RESULT 11
S18188
notch protein homolog - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 02-Aug-2002
C:Accession: S18188
R:Weinmaster, G.; Roberts, V.J.; Lemke, G.
Development 113, 199-205, 1991
A:Title: A homolog of Drosophila Notch expressed during mammalian development.
A:Reference number: S18188; MUID:92111383; PMID:1764995
A:Accession: S18188
A:Molecule type: mRNA
A:Residues: 1-2531 <WEI>
A:Cross-references: EMBL:X57405; NID:957634; PID:957635
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
F:987-1018/Domain: EGF homology <EGF1>
F:1025-1056/Domain: EGF homology <EGF2>
F:1233-1264/Domain: EGF homology <EGF2>
F:1917-1949/Domain: ankyrin repeat homology <AN1>
F:1950-1982/Domain: ankyrin repeat homology <AN2>
F:1984-2016/Domain: ankyrin repeat homology <AN3>
F:2017-2049/Domain: ankyrin repeat homology <AN4>
F:2050-2082/Domain: ankyrin repeat homology <AN5>
Alignment Scores:
Pred. No.: 0.151 Length: 2531
Score: 98.00 Matches: 41
Percent Similarity: 33.95% Conservative: 14
Best Local Similarity: 25.31% Mismatches: 56
Query Match: 11.04% Indels: 51
DB: 2 Gaps: 8
US-09-773-476-294 (1-489) x S18188 (1-2531)
QY 53 TTACAGGCTTATCTGCT-----ATTATCATAGACCTTCAG-----GCAATCTCT 97
Db 441 LeuGlnGlyTyThrGlyProArgCysGluIleAspValAsnGluCysIleSerAsnPro 460
QY 98 CTCAGAGATGATTTGGCCACACCTTCGGGGTTTACTCAGTCGACACTCTGATACTA 157
Db 461 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysIleCysMet 479
QY 158 CCA-----CAAGATGTTCCCTGT 175
Db 480 ProGlyTyGluGlyValTyCysGluIleAsnThrAspGluCysAlaSerProCys 499
QY 176 CTGGAGGTAGTAATGCTGGACAATGTTACTTCTTCAAG----- 217
Db 500 LeuHisAsnGlyArgCysValAspLysIleAsnGluPheLeuCysGlnCysProLysGly 519
QY 218 ---GACACAGCAGATTTGCCAAGGGCAAGGACCTTTGCAATAGCACTGGAAGCCCAGAA 274
Db 520 PheSerGlyHisLeuCysGlnTyAspValAspGluCysAlaSerThr----- 535

QY 275 ATGTGTCCTCAGACCGAATCTTTGGCACTGACGGTCCCTGGTCTTTTGACATGCCGTTTGT 334
 ||| :||:|||||:
 Db 536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys 554
 ||| :||:|||||:
 QY 335 GCTGATGTTTCCATGCATCAAACTG- - - - - 361
 ||| :||:|||||:
 Db 555 ThrGluGlyTyrThrGlyThrHisCysGluValAspIleAspGluCysAspProaspPro 574
 ||| :||:|||||:
 QY 362 -----ATGAGCAGCGGTCTCATTTTCACTGCTTTATGTTCTTTTGGG 400
 ||| :||:|||||:
 Db 575 CysHisIleGlyLeuCysLysAsp-GlyValAlaIatThrPheThrCysLeuCysGlnProGl 594
 ||| :||:|||||:
 QY 401 ATTC 404
 ||| :||:|||||:
 Db 594 Ytyr 595

RESULT 12
 T09059 notch4 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 08-Sep-2002
 C:Accession: T09059
 R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Laskey, S.; Lorentz,
 submitted to the EMBL Data Library, October 1997
 A:Description: Sequence of the mouse major histocompatibility locus class III
 A:Reference number: Z16543
 A:Accession: T09059
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1964 <ROW>
 A:Cross-references: EMBL:AF030001; NID:g2564945; PID:g2564947
 C:Genetics:
 A:Gene: notch4
 A:Map position: 17
 A:Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1;
 1675/3; 1729/1; 1761/3
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C:Keywords: receptor; signal transduction
 F:514-545/Domain: EGF homology <EGF>

Alignment Scores:			
Pred. No.:	0.172	Length:	1964
Score:	97.50	Matches:	34
Percent Similarity:	34.68%	Conservative:	9
Best Local Similarity:	27.42%	Mismatches:	43
Query Match:	10.98%	Indels:	38
DB:	2	Gaps:	6

US-09-773-476-294 (1-489) x T09059 (1-1964)

QY 128 GGTTTTACTCAGCTCAGACTCTGATACTACCACAAGATGTT-----CCCTGCTCT 178
 ||| :||:|||||:
 Db 264 GlyPheThrGlyLeuAspCysGluMetAsnProaspAspCysValArgHisGlnCysGln 283
 ||| :||:|||||:
 QY 179 GNGGTGTAGTAAGTCCTGGACAATCTTACTTCTTTCAG----- 217
 ||| :||:|||||:
 Db 284 AsnGlyAlaThrCysLeuAspGlyLeuAspThrTyrThrCysLeuCysProLysThrTrp 303
 ||| :||:|||||:
 QY 218 -----GACAAGCACAGATTTCGAAGGCGAAGGACCTTTTGCATATGACCTGGAAGC 268
 ||| :||:|||||:
 Db 304 LysGlyTrpAsp-----CysSerGluAspIleAspGluCysGluAlaArgGlyPro 320
 ||| :||:|||||:
 QY 269 CGAATAATGTCTCAGAACCGATCTTGTGCATCTGACGCTCTGCTCTTTTGCAGTGC 328
 ||| :||:|||||:
 Db 321 ProArg---CysArgAsnGlyThrCysGlnAsnThrAla---GlySerPheHisCys 338
 ||| :||:|||||:
 QY 329 GTTTGTGCTGATGGTTTCCATGCATCAAGTGTATG----- 364
 ||| :||:|||||:
 Db 339 ValCysValSerGlyTrpGlyAlaGlyCysGluGluAsnLeuAspCysAlaAla 358
 ||| :||:|||||:
 QY 365 -----AGCGAGGCGCTCATTTTCACTGCTTATG 391
 ||| :||:|||||:
 Db 359 AlaThrCysAlaProGlySerThrCysIleAspArgValGlySerPheSer-CysLeuCy 378
 ||| :||:|||||:
 Db 378 ---CysLeuAspGlySerPheSer-CysLeuCy 378

Qy	392	TTCTTTGGGA	401
Db	378	sProProGly	381

RESULT 13

A54785

preadipocyte factor 1 precursor, long form - mouse

N;Alternate names: delta-like dlk homeotic protein; pref-1

C;Species: Mus musculus (house mouse)

C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 02-Aug-2002

C;Accession: A54785; A5484; A40746; S21595

R;Smas, C.M.; Green, D.; Sul, H.S.

Biochemistry 33, 9257-9265, 1994

A;Title: Structural characterization and alternate splicing of the gene encoding the preadipocyte factor 1

A;Reference number: A54785; MUID:94325292; PMID:7515443

A;Accession: A54785

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-385 <SMA>

A;Cross-references: GB:S71340

R;Laborda, J.; Sauville, E.A.; Hoffman, T.; Notario, V.

J. Biol. Chem. 268, 3817-3820, 1993

A;Title: dlk, a putative mammalian homeotic gene differentially expressed in small cell cell carcinoma

A;Reference number: A45484; MUID:93179372; PMID:8095043

A;Accession: A45484

A;Molecule type: mRNA

A;Residues: 1-78, 'G', '80-343', 'TP', '346-385 <LAB>

A;Cross-references: EMBL:Z12171; NID:950716; PIDN:CAA78162.1; PID:G50717

A;Note: sequence extracted from NCBI backbone (NCBIP:125734)

A;Note: species designations for this sequence report and for B45484 originally were truncated

R;Smas, C.M.; Sul, H.S.

Cell 73, 725-734, 1993

A;Title: Pref-1, a protein containing EGF-like repeats, inhibits adipocyte differentiation

A;Reference number: A40746; MUID:93272313; PMID:8500166

A;Accession: A40746

A;Molecule type: mRNA

A;Residues: 1-78, 'G', '80-249, 'P', '251-319, 'CWAPWPSFSFSTSAKGCPTCATTCFARRRTSCCSITAARSWRSISSE

A;Cross-references: GB:I12721; NID:9305092; PIDN:AAA37175.1; PID:G309093

A;Experimental source: 3T3-L1 preadipocytes

A;Note: sequence extracted from NCBI backbone (NCBIN:132685, NCBIP:132713)

A;Note: this sequence appears to have been corrected in reference A45484

C;Superfamily: preadipocyte factor 1; EGF homology

C;Keywords: alternative splicing; tandem repeat; transmembrane protein

F;1-385/Product: preadipocyte factor 1 precursor splice form A #status predicted <FOA>

F;1-230,282-385/Product: preadipocyte factor 1 precursor splice form B #status predicted

F;1-230,304-385/Product: preadipocyte factor 1 precursor splice form C #status predicted

F;1-230,306-385/Product: preadipocyte factor 1 precursor splice form C2 #status predicted

F;1-210,304-385/Product: preadipocyte factor 1 precursor splice form D #status predicted

F;1-210,306-385/Product: preadipocyte factor 1 precursor splice form D2 #status predicted

F;92-124/Domain: EGF homology <EGF>

F;214-246/Domain: EGF homology <EGF1>

Alignment Scores:			
Pred. No.:	0.301	Length:	385
Score:	95.50	Matches:	33
Percent Similarity:	30.37%	Conservative:	8
Best Local Similarity:	24.44%	Mismatches:	45
Query Match:	10.75%	Indels:	49
DB:	2	Gaps:	4

US-09-773-476-294 (1-489) x A54785 (1-385)

Qy	133	TACTCAGCTGCAGACTCTGATACTACCAAGATGTTCCCTGCTGGAGGTACTAATGC	192
Db	34	TyrGlyPheCysGluAlaAspAsnValCysArgCysHisValGlyTrpGluGlyProLeu	53
Qy	193	CTGGGACAAATGTTACTTCTTCAAGA	222
Db	54	CysAspLysCysValThralaProGlyCysValAsnGlyValCysLysGluProTrpGln	73
Qy	223	GCAGATTTCGCAAGGCCAAGGGAC	255

Db 74 Cys-IleCysLysAspGlnTrpAspGlyLysPheCysGluIleAspValArgAlaCysTh 93
 QY 256 TAGCAGTGGAGCCAGCAAAATGCTCTGAGAACGGATCTTGTCATCTGACGGTCTCTG 315
 Db 93 rSerThr-----ProCysAlaAenAsnGlyThrCysValAspLeuGluysG 109
 QY 316 TCTTTTCAGTGGCTTTGTCTGCTGATGTTTCCATGATACAAAGTGTATGAGGAGGGCT- 374
 Db 109 YGlnTyrGluCysSerCysThrProGlyPheSerGlyLysAspCysGlnHis-LysAlaG 129
 QY 374 ----- 374
 Db 129 lyProCysValIleAenGlySerProCysGlnHisGlyLysAlaCysValAspAspGluG 149
 QY 375 -----CATTTTCACTGGTCTTATGTTCTTTTGGGATTC 404
 Db 149 lyGlnAlaSerHisAlaSerCysLeuCysProProGlyPhe 162

RESULT 14
 A35626
 transforming growth factor beta-1-binding protein - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Sep-1990 #sequence_revision 21-Sep-1990 #text_change 21-Jul-2003
 A:Accession: A35626
 R:Kanzaki, T.; Olofsson, A.; Moren, A.; Wernstedt, C.; Hellman, U.; Miyazono, K.; Claess
 Cell 61, 1051-1061, 1990
 A>Title: TGF-beta1 binding protein: a component of the large latent complex of TGF-beta1
 A:Reference number: A35626; PMID:90275601; PMID:2350783
 A:Accession: A35626
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-1394 <X>
 A:Cross-references: GB:M34057; NID:G339547; PIDN:AAA61160.1; PID:G339548
 C:Keywords: alternative splicing
 F:750-791/Domain: EGF homology <EGF>

Alignment Scores:
 Pred. No.: 0.277 Length: 1394
 Score: 95.50 Matches: 31
 Percent Similarity: 31.78% Conservative: 3
 Best Local Similarity: 28.97% Mismatches: 37
 Query Match: 10.75% Indels: 36
 DB: 2 Gaps: 4

US-09-773-476-294 (1-489) x A35626 (1-1394)
 QY 164 GATGTTCCCTGCTCTGGAGTAGTAATAGCTGGGCAATGTTACTTCTTTCAAGGACAAG 223
 Db 858 AspCysThrCysProAspGlyPheGlnLeuAspAspAsnLysThr----- 872
 QY 224 CAGATTGCCAAGGGCAAGGACCTTTCATAGCAGTGGAGCCAGAAATGTCTCT 283
 Db 873 -----CysGlnAsp-----IleAsnGluCysGluHisProGlyLeuCysGly 886
 QY 284 GAGAACGGATCTTGTCCATCTGACGGTCTCTGCTGTTTTCAGTGGCTTTGCTGATGTT 343
 Db 887 ProGlnGlyGluCysLeuAsnThr-----GluGlySerPheHisCysValCysGlnGlnGly 905
 QY 344 TTC----- 346
 Db 906 PheSerIleSerAlaAspGlyArgThrCysGluAspIleAspGluCysValAsnAsnThr 925
 QY 347 -----CATGGATACAAAGTGTATGACGAGCGGGCTCATTTTCACTGCTTATGTTTC 394
 Db 926 ValCysAspSerHisGlyPheCysAspAsnThrAlaGlySer-PheArgCysLeuCysTy 945
 QY 395 TTGGGATTCGGGATCCA 413
 Db 945 rGlnGlyPheGlnAlaPro 951

RESULT 15

T29234

hypothetical protein F55G1.13 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T29234
 R:Murray, J.; Le, T.T.
 submitted to the EMBL Data Library, May 1996
 A:Description: The sequence of C. elegans cosmid F55G1.
 A:Reference number: Z20591
 A:Accession: T29234
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-616 <MUR>
 A:Cross-references: EMBL:U58750; PIDN:AA00653.1; GSPDB:GN00022; CESP:F55G1.13
 A:Experimental source: strain Bristol N2; clone F55G1
 C:Genetics:
 A:Gene: CESP:F55G1.13
 A:Map position: 4
 A:Introns: 98/1; 136/1; 230/1; 256/1; 363/1; 401/1; 443/1; 484/1; 528/2; 551/3

Alignment Scores:
 Pred. No.: 0.327 Length: 616
 Score: 95.00 Matches: 36
 Percent Similarity: 38.71% Conservative: 12
 Best Local Similarity: 29.03% Mismatches: 43
 Query Match: 10.70% Indels: 33
 DB: 2 Gaps: 6

US-09-773-476-294 (1-489) x T29234 (1-616)
 QY 64 TACTGCTATTATCATAGACCTTCAGGCAATCTCTCAAGGATGATTTGGCCACACCTT 123
 Db 28 TyrCysIyr-----ProAlaAsnArgThrSerAlaThrThrCysSerGluCysThr 44
 QY 124 CCGTGGGTTTACTCAGCTGCAGACTCTGACTACTACC----- 159
 Db 45 CysSerAspGluSerThrGlnThrSerAspThrThrCysThrAlaProThrSerCysSer 64
 QY 160 ---ACAAGATGTTCCCTGCTCTGGAGGTAGTAATGCTGGGCAATGTTACTTCTTCAA 216
 Db 65 ProAsnProCysThrLeuSerAsnGln-----GlnCysAsnMetValAsn 79
 QY 217 GGACAAGCAGATTTCACAGGGCAAGGACCTTTCATAGCAGCTGGA----- 265
 Db 80 -----AspIleProThrCysThrCysAlaVal-GlyTyr-ThrGlyThrAspCysTh 96
 QY 266 -----AGCCCAAGAAATGTCTCTGAGAACGGATCTTGTGATC 303
 Db 96 rMetLeuThrSerAspProCysSerProGlnProCysLeuGlnAsnGlyValCysSerSe 116
 QY 304 TGACGGTCCCTGGTCTTTTGCAGTGGCTTTGCTGATGGTTTCCATGGATACAAAGTGTAT 363
 Db 116 rSerGly---GlyThrTyrSerCysAlaCysAlaThrGlyPhePheGlyGluGlnCysG 135
 QY 364 GAGCAGGGC 373
 Db 135 nTyrSerGly 138

Search completed: June 25, 2004, 09:17:56

Job time : 26 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 25, 2004, 09:09:32 ; Search time 14 Seconds
(without alignments)
3637.472 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 888
Sequence: 1 gactgaggctagattcttcag.....tnatgagccacacaaagactt 489

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Dalext 7.0	

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 283362

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-NODEL=frame_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US03773476/runat_25062004_090846_5816/app_query.fasta_1.647
-DB=SwissProt42 -Qfmt=fastan -SUFFIX=n2p.rsp -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORW=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09773476 @CGN 1 1 16 @runat_25062004_090846_5816 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_DSBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	113	12.7	2470	1 NTC2_MOUSE	O35516 mus musculus
2	112	12.6	2471	1 NTC2_RAT	Q9q30 rattus norv
3	103	11.6	2318	1 NTC3_MOUSE	Q61982 mus musculus
4	103	11.6	2531	1 NTC1_MOUSE	Q01705 mus musculus
5	102	11.5	2471	1 NTC2_HUMAN	Q04721 homo sapien
6	102	11.5	2703	1 NOTC_DROME	P07207 drosophila
7	101	11.4	2556	1 NTC1_HUMAN	P46531 homo sapien
8	100	11.3	2319	1 NTC3_RAT	Q9r172 rattus norv
9	99	11.1	1213	1 JAG3_BRARE	Q9y54 brachydanio
10	99	11.1	1964	1 NTC4_MOUSE	P31695 mus musculus
11	99	11.1	2003	1 NTC4_HUMAN	Q99466 homo sapien
12	98.5	11.1	1389	1 LTBS_MOUSE	Q8C918 mus musculus
13	98.5	11.1	1712	1 LTBI_RAT	Q00818 rattus norv
14	98.5	11.1	1713	1 LTBL_MOUSE	Q8C919 mus musculus
15	98.5	11.1	2321	1 NTC3_HUMAN	Q9um47 homo sapien
16	98	11.0	2531	1 NTC1_RAT	Q07008 rattus norv
17	96.5	10.9	1242	1 JAG1_BRARE	Q90y57 brachydanio
18	95.5	10.8	1394	1 LTBS_HUMAN	P22064 homo sapien

19	95.5	10.8	1595	1	LTBL_HUMAN	Q14766 homo sapien
20	95	10.7	675	1	PRTS_RAT	P53813 rattus norv
21	95	10.7	4391	1	PGSM_HUMAN	P98160 homo sapien
22	94.5	10.6	1218	1	JAG1_MOUSE	Q9qxx0 mus musculus
23	94.5	10.6	1219	1	JAG1_RAT	Q63722 rattus norv
24	94.5	10.6	2437	1	NTC1_BRARE	P46530 brachydanio
25	94	10.6	383	1	DLK_HUMAN	P80370 homo sapien
26	93.5	10.5	1218	1	JAG1_HUMAN	P78504 homo sapien
27	92.5	10.4	1238	1	JAG2_HUMAN	Q9y219 homo sapien
28	92.5	10.4	2524	1	NOTC_XENLA	P21783 xenopus lae
29	92.5	10.4	2907	1	FBN2_MOUSE	Q61555 mus musculus
30	92.5	10.4	2911	1	FBN2_HUMAN	P35556 homo sapien
31	92.5	10.4	4544	1	LRP1_HUMAN	Q07954 homo sapien
32	91.5	10.3	705	1	FBL1_MOUSE	Q08879 mus musculus
33	91.5	10.3	1202	1	JAG2_RAT	P97607 rattus norv
34	91.5	10.3	1247	1	JAG2_MOUSE	Q9q58 mus musculus
35	91	10.2	1408	1	SERR_DROME	P18168 drosophila
36	89.5	10.1	473	1	FP2_MYTGA	Q25464 mytilus gal
37	89	10.0	1064	1	FBP1_STRPU	P10079 strongyloce
38	89	10.0	2871	1	FBN1_PIG	Q9tv36 sus scrofa
39	88.5	10.0	385	1	DLK_MOUSE	Q09163 mus musculus
40	88.5	10.0	598	1	FBL1_CSERE	Q8mj99 cercopithec
41	88.5	10.0	1799	1	LMB2_MOUSE	Q61392 mus musculus
42	87.5	9.9	704	1	FBL1_CHICK	O73775 gallus gall
43	87	9.8	2871	1	FBN1_BOVIN	P98133 bos taurus
44	87	9.8	2871	1	FBN1_HUMAN	P35555 homo sapien
45	87	9.8	2871	1	FBN1_MOUSE	Q61554 mus musculus

ALIGNMENTS

RESULT 1
NTC2_MOUSE
ID NTC2_MOUSE STANDARD; PRT; 2470 AA.
AC O35516; Q06008; Q60941;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurogenic locus notch homolog protein 2 precursor (Notch 2) (Motch
DE B).
GN NOTCH2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Thymus;
RA Hamada Y., Higuchi M., Tsujimoto Y.;
RT "Complete amino acid sequence and multiform transcripts encoded by a
RT single copy of mouse Notch2 gene."
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 316-1518 FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Embryo;
RA MEDLINE=93178563; PubMed=8440332;
RX Lardelli M., Lendahl U.;
RT "Motch A and Motch B-two mouse Notch homologues coexpressed in a
RT wide variety of tissues."
RL Exp. Cell Res. 204:364-372(1993).
RN [3]
RP SEQUENCE OF 1765-2153 FROM N.A.
RX MEDLINE=97075110; PubMed=8917536;
RA Milner L.A., Bigas A., Kopan R., Brashem-Stein C., Bernstein I.D.,
RA Martin D.I.;
RT "Inhibition of granulocytic differentiation by mNotch1."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13014-13019(1996).
RN [4]
RP FUNCTION
RX MEDLINE=99396706; PubMed=10393120;
RA Hamada Y., Kadohawa Y., Okabe M., Ikawa M., Coleman J.R.,
RA Tsujimoto Y.;
RT "Mutation in ankyrin repeats of the mouse Notch2 gene induces early

embryonic lethality.";
Development 126:3415-3424 (1999).
[5]
RN DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
RX MEDLINE=95333893; PubMed=7609614;
RA Higuchi M., Kiyama H., Hayakawa T., Hanada Y., Tsujimoto Y.;
PT "Differential expression of Notch1 and Notch2 in developing and adult
mouse brain.";
RL Brain Res. Mol. Brain Res. 29:263-272 (1995).
[6]
RN POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
RX MEDLINE=21523956; PubMed=11518718;
RA Saxena M.T., Schroeter E.H., Mumm J.S., Kopan R.;
PT "Marine notch homologs (NL-4) undergo presenilin-dependent
proteolysis.";
RL J. Biol. Chem. 276:40268-40273 (2001).
[7]
RN POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS OF MET-1699.
RX MEDLINE=21374376; PubMed=11459941;
RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
PT "Conservation of the biochemical mechanisms of signal transduction
among mammalian Notch family members.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031 (2001).
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands
Jagged1, Jagged2 and Delta to regulate cell-fate determination.
Upon ligand activation through the released notch intracellular
domain (NICD) it forms a transcriptional activator complex with
RBP-J kappa and activates genes of the enhancer of split locus.
Affects the implementation of differentiation, proliferation and
apoptotic programs (By similarity). May play an essential role in
postimplantation development, probably in some aspect of cell
specification and/or differentiation.
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
terminal fragment N(EC) which are probably linked by disulfide
bonds.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
proteolytical processing NICD is translocated to the nucleus.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Names=1;
IsoId=O35516-1; Sequence=Displayed;
Names=2;
IsoId=O35516-2; Sequence=VSP_001405;
Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Expressed in the brain, liver, kidney,
neuroepithelia, somites, optic vesicles and branchial arches, but
not heart.
CC -!- DEVELOPMENTAL STAGE: Expressed in the embryonic ventricular zone,
the postnatal ependymal cells, and the choroid plexus throughout
embryonic and postnatal development.
CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
which is proteolytically cleaved by a furin-like convertase in the
trans-Golgi network before it reaches the plasma membrane to yield
an active, ligand-accessible form. Cleavage results in a C-
terminal fragment N(TM) and a N-terminal fragment N(EC). Following
ligand binding, it is cleaved by TNF-alpha converting enzyme
(TACE) to yield a membrane-associated intermediate fragment called
notch extracellular truncation (NEXT). This fragment is then
cleaved by presenilin dependent gamma-secretase to release a
notch-derived peptide containing the intracellular domain (NICD)
from the membrane.
CC -!- PTM: Phosphorylated.
CC -!- SIMILARITY: Belongs to the NOTCH family.
CC -!- SIMILARITY: Contains 35 EGF-like domains.
CC -!- SIMILARITY: Contains 2 lin/Notch repeats.
CC -!- SIMILARITY: Contains 6 ANK repeats.
CC
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch.

CC EMBL; D32210; BAA22094.1; -;
DR DEVELOPMENTAL STAGE, AND ALTERNATIVE SPLICING.
RX EMBL; X68279; CAA48340.1; -;
RA EMBL; U31881; AAC52924.1; -;
PT PIR; A49175; A49175.
DR HSSP; P16109; 1758.
DR MGD; MGI:97364; Notch2.
DR GO; GO:0005887; C:integral to plasma membrane; IC.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0002011; P:morphogenesis of an epithelial sheet; IMP.
DR GO; GO:0007219; P:N signaling pathway; IC.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001981; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008297; Notch.
DR InterPro; IPR000800; Notch_dom.
DR Pfam; PF00023; ank; 6.
DR Pfam; PF00008; EGF; 34.
DR Pfam; PF00066; notch; 2.
DR PIRSF; PIRSF002279; Notch; 1.
DR PRINTS; PR00010; EGFLOOD.
DR PRINTS; PR00011; EGFELAMININ.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00179; EGF_CA; 23.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 33.
DR PROSITE; PS01186; EGF_2; 27.
DR PROSITE; PS50026; EGF_3; 35.
DR PROSITE; PS01187; EGF_CA; 22.
KW Receptor; Transcription regulation; Activator; Differentiation;
KW Developmental protein; Repeat; ANK repeat; EGF-like domain;
KW Transmembrane; Glycoprotein; Signal; Phosphorylation;
KW Alternative splicing.
FT SIGNAL 1 25
FT CHAIN 26 2470 POTENTIAL.
FT CHAIN 1666 2470 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 2.
FT CHAIN 1697 2470 NOTCH EXTRACELLULAR TRUNCATION.
FT DOMAIN 26 1677 NOTCH INTRACELLULAR DOMAIN.
FT DOMAIN 26 1677 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1678 1698 POTENTIAL.
FT DOMAIN 1699 2470 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 26 63 EGF-LIKE 1.
FT DOMAIN 64 102 EGF-LIKE 2.
FT DOMAIN 105 143 EGF-LIKE 3.
FT DOMAIN 144 180 EGF-LIKE 4.
FT DOMAIN 182 219 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 221 256 EGF-LIKE 6 (INCOMPLETE).
FT DOMAIN 258 294 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 296 334 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 336 372 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 373 411 EGF-LIKE 10.
FT DOMAIN 413 452 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 454 490 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 492 528 EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 530 566 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 568 603 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 605 641 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 643 678 EGF-LIKE 17, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 680 716 EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 718 753 EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 755 791 EGF-LIKE 20, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 793 829 EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 831 869 EGF-LIKE 22, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 871 907 EGF-LIKE 23, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 909 945 EGF-LIKE 24, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN

FT	DOMAIN	947	983	EGF-LIKE 25,	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	985	1021	EGF-LIKE 26,	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1023	1059	EGF-LIKE 27,	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1061	1097	EGF-LIKE 28,	
FT	DOMAIN	1099	1145	EGF-LIKE 30,	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1147	1183	EGF-LIKE 31,	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1185	1221	EGF-LIKE 32,	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1223	1260	EGF-LIKE 33,	
FT	DOMAIN	1262	1300	EGF-LIKE 34,	
FT	DOMAIN	1302	1345	EGF-LIKE 35,	
FT	DOMAIN	1372	1410	LIN/NOTCH 1,	
FT	REPEAT	1418	1454	LIN/NOTCH 2,	
FT	REPEAT	1501	1533	ANK 1,	
FT	REPEAT	1825	1869		
Alignment Scores:					
Score, No.:	0.0012	Length:	2470		
Percent Similarity:	113.00	Matches:	38		
Best Local Similarity:	33.58%	Conservative:	7		
Query Match:	28.36%	Mismatches:	36		
DB:	12.73%	Indels:	53		
	1	Gaps:	6		
US-09-773-476-294 (1-489) x NTC2_MOUSE (1-2470)					
QY	98	CTCAAGGATGATTGGCCACACACCTTCGCTGGGTTTACTCAGTCGACACTCTGATACTA	157		
DB	910	IleAsnAspCysLeuAlaAsn	-----	916	
QY	158	CCACAAGATGTTCCCTGCTGGAGGTAGTATGCTCGGGACAATGTTACTTCTTCAAG	217		
DB	917	-----ProCysGlnAsnGlySerCysValAspHisValAsnThrPheSer	932		
QY	218	-----CACACAGCAGATTTCGCAAGGCGCAAGGACACTT	250		
DB	933	CysGlnCysHisProGlyPheIleGlyAspLys	-----CysGlnThrAspMetAsnGlu	950	
QY	251	TGCAATAGACATGGAGCCCGAAGATGTCCTGAGAACGATCTTGTCATCTTGACGGT	310		
DB	951	CysLeuSer	-----GluProCysLysAsnGlyGlyThrCys	965	
QY	311	CTGTGCTTTTGCAGTGGTTGTCTGATGTTTCCATGATACAACTGATGATGAGGAC	370		
DB	966	ValAsnSerTyThrCysThrCysProAlaGlyPheHisGlyValHisCysGluAsnAsn	985		
QY	371	-----	-----GGC	373	
DB	986	IleAspGluCysThrGluSerSerCysPheAsnGlyGlyThrCysValAspGlyIleAsn	1005		
QY	374	TCATTTCACCTTATGTTCTTCTGGATTCGGATCCA	413		
DB	1006	SerPheSer-CysLeuCysProValGlyPheThrGlyPro	1018		
RESULT 2					
ID	NTC2_RAT	STANDARD;	PRT;	2471	AA.
AC	O9QW30;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Neurogenic locus notch homolog protein 2 precursor (Notch 2).				
GN	NOTCH2.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RC	SEQUENCE FROM N.A.				
RP	TISSUE=Brain;				
RX	MEDLINE=93402015; PubMed=1295745;				
RA	Weinmaster G., Roberts V.J., Lemke G.;				
RT	"Notch2: a second mammalian Notch gene."				
RL	Development 116:931-941(1992).				

RN	TISSUE SPECIFICITY.
RP	MEDLINE=21331789; PubMed=11438922;
RX	Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;
RA	"Expression patterns of Notch1, Notch2, and Notch3 suggest multiple functional roles for the Notch-DSL signaling system during brain development."
RL	J. Comp. Neurol. 436:167-181(2001).
CC	-I- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta1 to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May play an essential role in postimplantation development, probably in some aspect of cell specification and/or differentiation (By similarity).
CC	-I- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide bonds (By similarity).
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.
CC	-I- TISSUE SPECIFICITY: Highly expressed in the spleen and choroid plexus in the brain. Expressed in postnatal central nervous system (CNS) germinal zones and, in early postnatal life, within numerous cells throughout the CNS. It is more highly localized to ventricular germinal zones. Also found in the heart, liver and kidney.
CC	-I- DEVELOPMENTAL STAGE: Expressed in the brain during E14 and E17.
CC	-I- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).
CC	-I- PTM: Phosphorylated (By similarity).
CC	-I- SIMILARITY: Belongs to the NOTCH family.
CC	-I- SIMILARITY: Contains 35 EGF-like domains.
CC	-I- SIMILARITY: Contains 2 Lin/Notch repeats.
CC	-I- SIMILARITY: Contains 6 ANK repeats.
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CC	EMBL; M93661; AAK13558.1; --
CC	PIR; A49128; A49128.
DR	HSSP; P00743; ICCF.
DR	InterPro; IPR002110; ANK.
DR	InterPro; IPR000152; Asx_hydroxyl_S.
DR	InterPro; IPR000742; EGF 2.
DR	InterPro; IPR001881; EGF_Ca.
DR	InterPro; IPR001438; EGF_II.
DR	InterPro; IPR006209; EGF-like.
DR	InterPro; IPR002049; Laminin_EGF.
DR	InterPro; IPR008297; Notch.
DR	InterPro; IPR008000; Notch_dom.
DR	Pfam; PF00023; ank; 6.
DR	Pfam; PF00008; EGF; 35.
DR	Pfam; PF00066; notch; 2.
DR	PIRSF; PIRSF002279; Notch; 1.
DR	PRINTS; PR00010; EGF_BLOOD.
DR	PRINTS; PR00011; EGFLAMININ.
DR	PRINTS; PR01452; NOTCH.

DR	SMART; SMO0248; ANK; 6.	90	FT	DISULFID	73	101	BY SIMILARITY.
DR	SMART; SMO0179; EGF CA; 24.	101	FT	DISULFID	92	121	BY SIMILARITY.
DR	SMART; SMO0004; NL; 2.	109	FT	DISULFID	109	131	BY SIMILARITY.
DR	PROSITE; PS00297; ANK REP REGION; 1.	115	FT	DISULFID	115	142	BY SIMILARITY.
DR	PROSITE; PS00088; ANK REPEAT; 4.	133	FT	DISULFID	133	159	BY SIMILARITY.
DR	PROSITE; PS00010; ASX HYDROXYL; 22.	148	FT	DISULFID	148	168	BY SIMILARITY.
DR	PROSITE; PS00022; EGF 1; 34.	153	FT	DISULFID	153	179	BY SIMILARITY.
DR	PROSITE; PS01186; EGF 2; 26.	170	FT	DISULFID	170	198	BY SIMILARITY.
DR	PROSITE; PS00026; EGF 3; 35.	186	FT	DISULFID	186	207	BY SIMILARITY.
DR	PROSITE; PS01187; EGF CA; 22.	192	FT	DISULFID	192	218	BY SIMILARITY.
KW	Receptor; Transcription regulation; Activator; Differentiation;	209	FT	DISULFID	209	236	BY SIMILARITY.
KW	Developmental protein; Repeat; ANK repeat; EGF-like domain;	225	FT	DISULFID	225	246	BY SIMILARITY.
KW	Transmembrane; Glycoprotein; Signal; Phosphorylation.	230	FT	DISULFID	230	257	BY SIMILARITY.
FT	SIGNAL	248	FT	DISULFID	248	275	BY SIMILARITY.
FT	CHAIN	264	FT	DISULFID	264	284	BY SIMILARITY.
FT	CHAIN	269	FT	DISULFID	269	295	BY SIMILARITY.
FT	CHAIN	286	FT	DISULFID	286	315	BY SIMILARITY.
FT	CHAIN	302	FT	DISULFID	302	324	BY SIMILARITY.
FT	CHAIN	309	FT	DISULFID	309	335	BY SIMILARITY.
FT	CHAIN	326	FT	DISULFID	326	353	BY SIMILARITY.
FT	CHAIN	342	FT	DISULFID	342	362	BY SIMILARITY.
FT	CHAIN	347	FT	DISULFID	347	373	BY SIMILARITY.
FT	CHAIN	364	FT	DISULFID	364	390	BY SIMILARITY.
FT	CHAIN	379	FT	DISULFID	379	401	BY SIMILARITY.
FT	CHAIN	384	FT	DISULFID	384	412	BY SIMILARITY.
FT	CHAIN	403	FT	DISULFID	403	433	BY SIMILARITY.
FT	CHAIN	419	FT	DISULFID	419	442	BY SIMILARITY.
FT	CHAIN	427	FT	DISULFID	427	453	BY SIMILARITY.
FT	CHAIN	444	FT	DISULFID	444	471	BY SIMILARITY.
FT	CHAIN	460	FT	DISULFID	460	480	BY SIMILARITY.
FT	CHAIN	465	FT	DISULFID	465	491	BY SIMILARITY.
FT	CHAIN	482	FT	DISULFID	482	498	BY SIMILARITY.
FT	CHAIN	498	FT	DISULFID	498	509	BY SIMILARITY.
FT	CHAIN	503	FT	DISULFID	503	518	BY SIMILARITY.
FT	CHAIN	520	FT	DISULFID	520	529	BY SIMILARITY.
FT	CHAIN	536	FT	DISULFID	536	547	BY SIMILARITY.
Alignment Scores:							
Pred. No.:				Length:			
Score:				Matches:			
Percent Similarity:				Conservative:			
Best Local Similarity:				Mismatch:			
Query Match:				Indels:			
DB:				Gaps:			
US-09-773-476-294 (1-489) x NTC2_RAT (1-2471)				0.00153			
QY				98			
Db				912			
QY				158			
Db				919			
QY				218			
Db				935			
QY				251			
Db				953			
QY				311			
Db				968			
QY				371			
Db				988			
QY				374			

FT	DOMAIN	963	999	EGF-LIKE 25.	
FT	DOMAIN	1001	1035	EGF-LIKE 26.	
FT	DOMAIN	1037	1083	EGF-LIKE 27.	
FT	DOMAIN	1085	1121	EGF-LIKE 28.	
FT	DOMAIN	1123	1159	EGF-LIKE 29.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1161	1204	EGF-LIKE 30.	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	1206	1245	EGF-LIKE 31.	
FT	DOMAIN	1247	1288	EGF-LIKE 32.	
FT	DOMAIN	1290	1326	EGF-LIKE 33.	
FT	DOMAIN	1336	1374	EGF-LIKE 34.	
FT	REPEAT	1388	1428	LIN/NOTCH 1.	
FT	REPEAT	1429	1467	LIN/NOTCH 2.	
FT	REPEAT	1468	1503	LIN/NOTCH 3.	
FT	REPEAT	1839	1868	ANK 1.	
FT	REPEAT	1872	1902	ANK 2.	
FT	REPEAT	1906	1935	ANK 3.	
FT	REPEAT	1939	1968	ANK 4.	
FT	REPEAT	1972	2001	ANK 5.	
FT	SITE	1572	1573	CLEAVAGE (BY FURIN-LIKE PROTEASE) (BY SIMILARITY).	
FT	DISULFID	43	55	BY SIMILARITY.	
FT	DISULFID	49	66	BY SIMILARITY.	
FT	DISULFID	68	77	BY SIMILARITY.	
FT	DISULFID	83	94	BY SIMILARITY.	
FT	DISULFID	88	107	BY SIMILARITY.	
FT	DISULFID	109	118	BY SIMILARITY.	
FT	DISULFID	124	135	BY SIMILARITY.	
FT	DISULFID	129	145	BY SIMILARITY.	
FT	DISULFID	147	156	BY SIMILARITY.	
FT	DISULFID	163	175	BY SIMILARITY.	
FT	DISULFID	169	184	BY SIMILARITY.	
FT	DISULFID	186	195	BY SIMILARITY.	
FT	DISULFID	202	213	BY SIMILARITY.	
FT	DISULFID	207	223	BY SIMILARITY.	
FT	DISULFID	225	234	BY SIMILARITY.	
FT	DISULFID	241	252	BY SIMILARITY.	
FT	DISULFID	246	261	BY SIMILARITY.	
FT	DISULFID	263	272	BY SIMILARITY.	
FT	DISULFID	279	292	BY SIMILARITY.	
FT	DISULFID	286	301	BY SIMILARITY.	
FT	DISULFID	303	312	BY SIMILARITY.	
FT	DISULFID	319	330	BY SIMILARITY.	
FT	DISULFID	324	339	BY SIMILARITY.	
FT	DISULFID	341	350	BY SIMILARITY.	
FT	DISULFID	356	367	BY SIMILARITY.	
FT	DISULFID	361	378	BY SIMILARITY.	
FT	DISULFID	380	389	BY SIMILARITY.	
FT	DISULFID	396	409	BY SIMILARITY.	
FT	DISULFID	403	418	BY SIMILARITY.	
FT	DISULFID	420	429	BY SIMILARITY.	
FT	DISULFID	436	447	BY SIMILARITY.	
FT	DISULFID	441	456	BY SIMILARITY.	
FT	DISULFID	458	467	BY SIMILARITY.	
FT	DISULFID	474	485	BY SIMILARITY.	
FT	DISULFID	479	494	BY SIMILARITY.	
FT	DISULFID	496	505	BY SIMILARITY.	
FT	DISULFID	512	523	BY SIMILARITY.	
FT	DISULFID	517	532	BY SIMILARITY.	
Alignment Scores:					
Pred. No.:		0.0135	Length:	2318	
Score:		103.00	Matches:	28	
Percent Similarity:		40.62%	Conservative:	11	
Best Local Similarity:		29.17%	Mismatches:	21	
Query Match:		11.60%	Indels:	36	
DB:		1	Gaps:	6	
US-09-773-476-294 (1-489) x NTC3_MOUSE (1-2318)					
Qy	140	CTCAGACTCTGATCTACACAGATGTCCTCTGT	-----	175	
Db	689	LeuProProLeuCysLeuProAlaAsnHisProCysAlaHisLysProCysSerHisGly	-----	708	

QY	176	-----CCTGGAGGTAGTAATGCTCGGACAAATGTTACTTCTTCAAGGAC	220	
Db	709	ValCysHisAspAlaProGlyGlyPheArgCys	719	
QY	221	RAGCAGATTTCGCA	-----GGCAAGGACCTTTGCAATAGCAGCTGGAAGC	268
Db	720	-----ValCysGluProGlyTrpSerGlyProArg	-----CysSerGlnSerLeuAla	735
QY	269	CCAGAAATGTCCTCTGAG	-----AACGGATCTTGTGCACTCTGACGGTCTCT	313
Db	736	ProAspAlaCysGluSerGlnProCysGlnAlaGlyGlyThrCysThrSerAspGlyIle	755	
QY	314	GGTCTTTTGCAGTCGGTTTGTCTGATGCTTTCATGATACAAAGTGT	361	
Db	756	Gly-----PheArgCysThrCysAlaProGlyPheGlnGlyHisGlnCys	770	
RESULT 4				
ID	NTC1_MOUSE	STANDARD;	PRT;	2531 AA.
AC	Q01705; Q06007; Q61905; Q99JC2; Q9QM58; Q9R0X7;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Notch A)			
DE	(M714) (p300).			
GN	NOTCH1 OR NOTCH.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1] _SEQUENCE FROM N.A. (ISOFORM 1).			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Embryo;			
RX	MEDLINE=93194170; PubMed=8449489;			
RA	Franco del Amo F., Gendron-Maguire M., Swiatek P.J., Jenkins N.A.,			
RA	Copeland N.G., Gridley T.;			
RT	"Cloning, analysis, and chromosomal localization of Notch-1, a mouse			
RT	homolog of Drosophila Notch.;"			
RL	Genomics 15:259-264(1993).			
RN	[2]			
RP	SEQUENCE OF 731-1899 FROM N.A. (ISOFORM 2), AND DEVELOPMENTAL STAGE.			
RC	STRAIN=CD-1; TISSUE=Embryo;			
RX	MEDLINE=93050801; PubMed=1426644;			
RA	Reaume A.G., Conlon R.A., Zirngibl R., Yamaguchi T.P., Rossant J.;			
RT	"Expression analysis of a Notch homologue in the mouse embryo.;"			
RL	Dev. Biol. 154:377-387(1992).			
RN	[3]			
RP	SEQUENCE OF 1551-1647 FROM N.A. (ISOFORM 1), AND DEVELOPMENTAL STAGE.			
RC	TISSUE=Embryo;			
RX	MEDLINE=93048835; PubMed=1425352;			
RA	Franco del Amo F., Smith D.E., Swiatek P.J., Gendron-Maguire M.,			
RA	Greenspan R.J., McMahon A.P., Gridley T.;			
RT	"Expression pattern of Notch, a mouse homolog of Drosophila Notch,			
RT	suggests an important role in early postimplantation mouse			
RT	development.;"			
RL	Development 115:737-744(1992).			
RN	[4]			
RP	SEQUENCE OF 1161-1547 FROM N.A.			
RC	STRAIN=C57BL/6 X CBA; TISSUE=Embryo;			
RX	MEDLINE=93178563; PubMed=8440332;			
RA	Lardelli M., Lendahl U.;			
RT	"Notch A and Notch B-two mouse Notch homologues coexpressed in a			
RT	wide variety of tissues.;"			
RL	Exp. Cell Res. 204:364-372(1993).			
RN	[5]			
RP	SEQUENCE OF 1659-1673 FROM N.A.			
RX	MEDLINE=93364499; PubMed=10437788;			
RA	Lee J.S., Ishimoto A., Yanagawa S.I.;			
RT	"Murine leukemia provirus-mediated activation of the Notch1 gene leads			
RT	to induction of HES-1 in a mouse T lymphoma cell line, DU-3.;"			
RL	FEBS Lett. 455:276-280(1999).			
RN	[6]			
RP	SEQUENCE OF 1950-2201 FROM N.A.			

Alignment Scores: 0.0137 Length: 2531
 Pred. No.: 103.00 Matches: 41
 Score: 103.00 Conservative: 17
 Percent Similarity: 35.80% Mismatches: 53
 Best Local Similarity: 25.31% Indels: 51
 Query Match: 11.60% Gaps: 8
 DB: 1

US-09-773-476-294 (1-489) x NTC1_MOUSE (1-2531)

QY 53 TTACAGGCTTATCT-----GCTATTATCATAGACCTTCAG-----GGAATTCCT 97
 Db 441 LeuGlnGlyThrGlyProGlyCysGluLeuAspValAsnGluCysIleSerAsnPro 460
 QY 98 CTCAGAGATGTTGGCAACACCTTCGGGGTTCCTACTCAGTCGAGACTCTGTACTA 157
 Db 461 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysIleCysMet 479
 QY 158 CCA-----CAAGATGTTCCCTGT 175
 Db 480 ProGlyTyrgluGlyValTyrcysGluLeuAsnThrAspGluCysAlaSerSerProCys 499
 QY 176 CCTGGAGTGTATGCTGGCAACATGTTACTTCTTTCAAG----- 217
 Db 500 LeuHisAsnGlyHisCysMetAspLysIleHisGluPheGlnCysGlnCysProLysGly 519
 QY 218 ---CACAGCAGATTGCCAGGCAAGGACCTTTCGATAGCAGCTCGAAGCCAGAA 274
 Db 520 PheAsnGlyHisLeuCysGlnTyrcysValAspGluCysAlaSerThr----- 535
 QY 275 ATGTCCTCTCAGACGAGATCTTGTCATCTCAGCGTCTCGTCTTTTGCAGTCGCTTGT 334
 Db 536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrcysValCys 554
 QY 335 GCTCATGTTCCATGATACAGTGT----- 361
 Db 555 ThrGluGlyTyrcysGlyThrHisCysGluValAspLeuAspGluCysAspProAspPro 574
 QY 362 -----ATCAGCAGGCTCATTTTCACTGCTTATGTTCTTTGG 400
 Db 575 CysHisTyrcysGlySerCysLysAsp-GlyValAlaThrPheThrCysLeuCysGlnProGln 594
 QY 401 ATTC 404
 Db 594 yTyr 595

RESULT 5
 NTC2 HUMAN
 ID NTC2_HUMAN STANDARD; PRT; 2471 AA.
 AC Q04721; Q99734; Q9H240;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Neurogenic locus notch homolog protein 2 precursor (Notch 2) (hN2).
 GN NOTCH2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Blaumüller C.M., Mann R.S.;
 RT "Complete human notch 2 (hN2) cDNA sequence."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast tumor;
 RA Correa R.G., Camargo A.A., Moreira E.S., Simpson A.J.G.;
 RT "Human Notch2, a novel member of cell-fate determining NOTCH family."
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]

SEQUENCE OF 967-1229 FROM N.A.
 TISSUE=T-cell;
 Lemasson I., Devaux C., Mesnard J.M.;
 "Partial sequence of EGF-like repeat domain of human Notch2 mRNA."
 Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 (4)
 SEQUENCE OF 1810-2447 FROM N.A.
 TISSUE=Brain;
 MEDLINE=93265135; PubMed=1303260;
 Stifani S., Blaumüller C.M., Redhead N.J., Hill R.E.,
 Artavanis-Tsakonas S.;
 "Human homologs of a Drosophila enhancer of split gene product define
 a novel family of nuclear proteins."
 Nat. Genet. 2:119-127(1992).
 (5)
 POST-TRANSLATIONAL PROCESSING.
 MEDLINE=97386453; PubMed=9244302;
 Blaumüller C.M., Qi H., Zagouras P., Artavanis-Tsakonas S.;
 "Intracellular cleavage of Notch leads to a heterodimeric receptor on
 the plasma membrane."
 Cell 90:281-291(1997).
 (6)
 IDENTIFICATION OF LIGANDS.
 MEDLINE=99180765; PubMed=10079256;
 Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
 Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
 "Human ligands of the Notch receptor."
 Am. J. Pathol. 154:785-794(1999).
 CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands
 Jagged1, Jagged2 and Delta to regulate cell-fate determination.
 Upon ligand activation through the released notch intracellular
 domain (NICD) it forms a transcriptional activator complex with
 RBP-J kappa and activates genes of the enhancer of split locus.
 Affects the implementation of differentiation, proliferation and
 apoptotic programs (By similarity).
 CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
 terminal fragment N(EC) which are probably linked by disulfide
 bonds (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
 proteolytical processing NICD is translocated to the nucleus.
 CC -!- TISSUE SPECIFICITY: Expressed in the brain, heart, kidney, lung,
 skeletal muscle and liver.
 CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 which is proteolytically cleaved by a furin-like convertase in the
 trans-Golgi network before it reaches the plasma membrane to yield
 an active, ligand-accessible form. Cleavage results in a C-
 terminal fragment N(TM) and a N-terminal fragment N(EC). Following
 ligand binding, it is cleaved by TNF-alpha converting enzyme called
 (TACE) to yield a membrane-associated intermediate fragment called
 notch extracellular truncation (NEXT). This fragment is then
 cleaved by presenilin dependent gamma-secretase to release a
 notch-derived peptide containing the intracellular domain (NICD)
 from the membrane (By similarity).
 CC -!- PTM: Phosphorylated (By similarity).
 CC -!- SIMILARITY: Belongs to the NOTCH family.
 CC -!- SIMILARITY: Contains 35 EGF-like domains.
 CC -!- SIMILARITY: Contains 2 Lin/Notch repeats.
 CC -!- SIMILARITY: Contains 6 ANK repeats.
 CC -----
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 EMBL; AF308601; AAA36377.2; -;
 EMBL; AF315356; AAG37073.1; -;
 EMBL; U77493; AAB19224.1; -;
 HSSP; P00740; 1EDM.
 Genew; HGNC:7882; NOTCH2.
 MIM; 600275; -;

NOTC DROME STANDARD; PRT: 2703 AA.
 ID NOTC DROME STANDARD; PRT: 2703 AA.
 AC P07207; 097458; P04154; Q9W4T8;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neurogenic locus Notch protein precursor.
 GN N OR EG:140611.1 OR EG:163A10.2 OR CG3936.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R; TISSUE=Embryo;
 RX MEDLINE=86079539; PubMed=3935325;
 RA Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.;
 RT "Nucleotide sequence from the neurogenic locus notch implies a gene
 RT product that shares homology with proteins containing EGF-like
 RT repeats.";
 RL Cell 43:567-581 (1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S, and Oregon-R; TISSUE=Embryo;
 RX MEDLINE=87064624; PubMed=3097517;
 RA Kidd S., Kelley M.R., Young M.W.;
 RT "Sequence of the notch locus of Drosophila melanogaster: relationship
 RT of the encoded protein to mammalian clotting and growth factors.";
 RL Mol. Cell. Biol. 6:3094-3108 (1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champé M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Frankkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Burtis K.C., Buzan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlike C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ithegawam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN [4]

SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RX MEDLINE=20196011; PubMed=10731137;
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
 RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
 RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
 RA Minano B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
 RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
 RA McDevell J., Peter A., Schoettler P., Werner M., Mourikioti F.,
 RA Beinert N., Dowe G., Schaefer U., Jaackle H., Bucheton A.,
 RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
 RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
 RA Glover D.M.;
 RT "From sequence to chromosome: the tip of the X chromosome of D.
 RT melanogaster.";
 RL Science 287:2220-2222 (2000).
 RN [5]
 RP SEQUENCE OF 2505-2611 FROM N.A.
 RX MEDLINE=85093929; PubMed=2981631;
 RA Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;
 RT "opa: a novel family of transcribed repeats shared by the Notch locus
 RT and other developmentally regulated loci in D. melanogaster.";
 RL Cell 40:55-62 (1985).
 RN [6]
 RP SEQUENCE OF 1-8 FROM N.A.
 RX MEDLINE=87257846; PubMed=3037327;
 RA Kelley M.R., Kidd S., Berg R.L., Young M.W.;
 RT "Restriction of P-element insertions at the Notch locus of Drosophila
 RT melanogaster.";
 RL Mol. Cell. Biol. 7:1545-1548 (1987).
 RN [7]
 RP INTERACTION WITH DX AND MUTANT SU42C.
 RX MEDLINE=94215489; PubMed=8162048;
 RA Diederich R.J., Matsuno K., Hing H., Artavanis-Tsakonas S.;
 RT "Cytosolic interaction between deltex and Notch ankyrin repeats
 RT implicates deltex in the Notch signaling pathway.";
 RL Development 120:473-481 (1994).
 RN [8]
 RP INTERACTION WITH DX.
 RX MEDLINE=95401878; PubMed=7671825;
 RA Matsuno K., Diederich R.J., Go M.J., Blaumueller C.M.,
 RA Artavanis-Tsakonas S.;
 RT "Deltex acts as a positive regulator of Notch signaling through
 RT interactions with the Notch ankyrin repeats.";
 RL Development 121:2633-2644 (1995).
 RN [9]
 RP S3 CLEAVAGE BY PSN.
 RX MEDLINE=99221487; PubMed=102066646;
 RA Struhl G., Greenwald I.;
 RT "Presenilin is required for activity and nuclear access of Notch in
 RT Drosophila.";
 RL Nature 398:522-525 (1999).
 RN [10]
 RP S3 CLEAVAGE BY PSN.
 RX MEDLINE=99221488; PubMed=102066647;
 RA Ye Y., Lukinova N., Fortini M.E.;
 RT "Neurogenic phenotypes and altered Notch processing in Drosophila
 RT Presenilin mutants.";
 RL Nature 398:525-529 (1999).
 RN [11]
 RP S2 CLEAVAGE BY KUZ.
 RX MEDLINE=21657146; PubMed=11799064;
 RA Lieber T., Kidd S., Young M.W.;
 RT "kuzbanian-mediated cleavage of Drosophila Notch.";
 RL Genes Dev. 16:209-221 (2002).
 RN [12]
 RP MUTANT MCD5.
 RX MEDLINE=21575956; PubMed=11719214;
 RA Ramin P., Knechumian K., Seugnet L., Arbogast N., Ackermann C.,
 RA Heitzler P.;
 RT "Novel Notch alleles reveal a Deltex-dependent pathway repressing
 RT neural fate.";
 RL Curr. Biol. 11:1729-1738 (2001).

RP MEDLINE=22256570; PubMed=12369105;
RA Portin P.;
RT "General outlines of the molecular genetics of the Notch signalling
pathway in Drosophila melanogaster: a review.";
RL Hereditas 136:89-96(2002).
CC -!- FUNCTION: Signaling protein, which regulates, with both positive
and negative signals, the differentiation of at least central and
peripheral nervous system and eye, wing disk, oogenesis, segmental
appendages such as antennae and legs, and muscles, through lateral
inhibition or induction. Functions as a receptor for membrane-
bound ligands Delta and Serrate to regulate cell-fate
determination. Upon ligand activation, and releasing from the cell
membrane, the Notch intracellular domain (NICD) forms a
transcriptional activator complex with Su(H) (suppressor of
hairless) and activates genes of the E(spl) complex. Essential for
proper differentiation of ectoderm.
CC -!- SUBUNIT: Interacts with Su(H) when activated. Interacts with Dx
via its ANK repeats.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Upon activation and
S3 cleavage, it is released from the cell membrane and enters into
the nucleus in conjunction with Su(H).
CC -!- PTM: Upon binding its ligands such as Delta or Serrate, it is
cleaved (S2 cleavage) in its extracellular domain, close to the
transmembrane domain. S2 cleavage is probably mediated by Kuz. It
is then cleaved (S3 cleavage) downstream of its transmembrane
domain, releasing it from the cell membrane. S3 cleavage requires
Psn.
CC -!- SIMILARITY: Belongs to the NOTCH family.
CC -!- SIMILARITY: Contains 36 EGF-like domains.
CC -!- SIMILARITY: Contains 3 Lin/Notch repeats.
CC -!- SIMILARITY: Contains 6 ANK repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
DR EMBL; M16152; AAB59220.1; -
DR EMBL; M16153; AAB59220.1; JOINED.
DR EMBL; M16149; AAB59220.1; JOINED.
DR EMBL; M16150; AAB59220.1; JOINED.
DR EMBL; M16151; AAB59220.1; JOINED.
DR EMBL; K03508; AAB28725.1; -
DR EMBL; K03509; AAB28725.1; JOINED.
DR EMBL; M13689; AAA28725.1; JOINED.
DR EMBL; K03507; AAA28725.1; JOINED.
DR EMBL; AE003426; AAF45848.2; -
DR EMBL; AL035436; CAB37610.1; -
DR EMBL; AL035395; CAB37610.1; JOINED.
DR EMBL; M12175; AA74496.1; -
DR EMBL; M16025; AAA28726.1; -
Alignment Scores:
Pred. No.: 0.0177 Length: 2703
Score: 102.00 Matches: 25
Percent Similarity: 42.25% Conservative: 5
Best Local Similarity: 35.21% Mismatches: 29
Query Match: 11.49% Indels: 12
DB: 1 Gaps: 3
US-09-773-476-294 (1-489) x NOTC_DROME (1-2703)
QY 170 CCTGTCCTGAGTAGTATGCTGGCAATGTTACTTCTTTCAAGGACAG----- 223
Db 1229 ProCysGlnAsnGlyThrCysHisAspArgValMetAsnPheSerCysSerCysPro 1248
QY 224 -----CAGATTTCGCAAGGCGCAAGGACCTTTGCAATAGCAGC 268
Db 1249 ProGlyThrMetGlyIleIleCysGluIleAsnLysAspCys-----Lys 1264

QY 269 CCAGAAATGTCTCTGAGAACGATCTTGTGCATCTGACGGTCTGCTGCTTTTTCAGTGC 328
Db 1265 ProGlyAlaCysHisAsnGlySerCysIle---AspArgValGlyGlyPheGluCys 1283
QY 329 GTTTGTGCTGATGGTTTCCATGATGATCAAGTGT 361
Db 1284 ValCysGlnProGlyPheValGlyAlaArgCys 1294
RESULT 7
NTCL HUMAN STANDARD; PRT; 2556 AA.
ID NTCL HUMAN AC P46531;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurogenic locus notch homolog protein 1 precursor (Notch 1) (hnl)
DE (Translocation-associated notch protein TAN-1).
GN NOTCH1 OR TANI.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CN NCBI_TaxID=9606;
[1]
RC TISSUE=Brain;
RA Mann R.S., Blaumüller C.M., Zagouras P.;
RT "Complete human notch 1 (hnl) cDNA sequence.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE OF 1-2444 FROM N.A.
RP MEDLINE=91347367; PubMed=1831692;
RA Ellisen L.W., Bird J., West D.C., Soreng A.L., Reynolds T.C.,
RA Smith S.D., Sklar J.;
RT "TAN-1, the human homolog of the Drosophila notch gene, is broken by
chromosomal translocations in T lymphoblastic neoplasms.";
RL Cell 66:649-661(1991).
[3]
RP IDENTIFICATION OF LIGANDS.
RX MEDLINE=99180765; PubMed=10079256;
RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.L.,
RA Banks A., Leiman J., Ward D., Ieh-Horowitz D., Artavanis-Taikonas S.;
RT "Human ligands of the Notch receptor.";
RL Am. J. Pathol. 154:785-794(1999).
[4]
RP INTERACTION WITH DTX1.
RX MEDLINE=98250176; PubMed=9590294;
RA Matsuno K., Eastman D., Mitsiadis E., Carcangiu M.L.,
RA Ordentlich P., Kadesch T., Artavanis-Taikonas S.;
RT "Human deltex is a conserved regulator of Notch signalling.";
RL Nat. Genet. 19:74-78(1998).
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands
Jagged1, Jagged2 and Deltal to regulate cell-fate determination.
CC Upon ligand activation through the released notch intracellular
domain (NICD) it forms a transcriptional activator complex with
RBP-J kappa and activates genes of the enhancer of split locus.
CC Affects the implementation of differentiation, proliferation and
apoptotic programs. May be important for normal lymphocyte
function. In altered form, may contribute to transformation or
progression in some T-cell neoplasms. Involved in the maturation
of both CD4+ and CD8+ cells in the thymus (By similarity).
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
terminal fragment N(EC) which are probably linked by disulfide
bonds (By similarity). Interacts with DTX1 and DTX2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
proteolytical processing NICD is translocated to the nucleus (By
similarity).
CC -!- TISSUE SPECIFICITY: In fetal tissues most abundant in spleen,
brain stem and lung. Also present in most adult tissues where it
is found mainly in lymphoid tissues.
CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
which is proteolytically cleaved by a furin-like convertase in the
trans-Golgi network before it reaches the plasma membrane to yield

an active, ligand-accessible form. Cleavage results in a C-terminal fragment (NTM) and a N-terminal fragment (NEC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (by similarity).

-!- PFM: Phosphorylated (by similarity).

-!- DISEASE: NOTCH1 truncation is associated with T-cell acute lymphoblastic leukemia.

-!- SIMILARITY: Belongs to the NOTCH family.

-!- SIMILARITY: Contains 36 EGF-like domains.

-!- SIMILARITY: Contains 3 Lin/Notch repeats.

-!- SIMILARITY: Contains 5 ANK repeats.

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EMBL; AF308602; AAG33848.1; --

EMBL; M73980; AAA60614.1; --

HSSP; P00740; LEDM

Genew; HGNC:7881; NOTCH1.

MIM; 190198; --

GO; GO:0016021; C: integral to membrane; NAS.

GO; GO:0003793; F: defense/immunity protein activity; NAS.

GO; GO:0006955; P: immune response; NAS.

InterPro; IPR002110; ANK.

InterPro; IPR000152; Asx_hydroxyl_S.

InterPro; IPR000742; EGF_2.

InterPro; IPR001881; EGF_Ca.

InterPro; IPR001438; EGF_II.

InterPro; IPR006209; EGF_Like.

InterPro; IPR002049; Laminin_EGF.

InterPro; IPR008297; Notch.

InterPro; IPR008000; Notch_dom.

Pfam; PF00023; ank; 6.

Pfam; PF00008; EGF; 35.

Pfam; PF00066; notch; 3.

PIRSF; PIRSF002279; Notch; 1.

PRINTS; PR00010; EGFBL00D.

PRINTS; PR00011; EGFLAMININ.

PRINTS; PR01452; NOTCH.

SMART; SM00248; ANK; 6.

SMART; SM00179; EGF_CA; 23.

SMART; SM00004; NL; 3.

PROSITE; PS50297; ANK_REPEAT_REGION; 1.

PROSITE; PS50088; ANK_REPEAT; 4.

PROSITE; PS00010; ASX_HYDROXYL; 20.

PROSITE; PS00022; EGF_1; 34.

PROSITE; PS01186; EGF_2; 26.

PROSITE; PS50026; EGF_3; 36.

PROSITE; PS01187; EGF_CA; 18.

Receptor; Transcription regulation; Activator; Differentiation; Developmental protein; Repeat; ANK repeat; EGF-like domain; Transmembrane; Glycoprotein; Signal; Phosphorylation.

SIGNAL 1 18

CHAIN 19 2556

FT CHAIN 1722 2556

FT CHAIN 1755 2556

FT CHAIN 1736 2556

FT CHAIN 1737 1757

FT CHAIN 1758 2556

FT CHAIN 20 58

FT CHAIN 59 99

FT CHAIN 102 139

DOMAIN 19 1736

DOMAIN 1737 1757

DOMAIN 1758 2556

DOMAIN 20 58

DOMAIN 59 99

DOMAIN 102 139

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

EGF-Like 1.

EGF-Like 2.

EGF-Like 3.

140 DOMAIN

178 DOMAIN

218 DOMAIN

257 DOMAIN

293 DOMAIN

333 DOMAIN

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Alignment Scores:

Pred. No.: 0.0224

Score: 101.00

Percent Similarity: 35.19%

Best Local Similarity: 25.31%

Query Match: 11.37%

DB: 1

Length: 2556

Matches: 41

Conservative: 16

Mismatches: 54

Indels: 51

Gaps: 8


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US-09-773-476-294 (1-489) x NTC1_HUMAN (1-2556)
QY 53 TTACAGGCTTACTGCT-----ATTATCATAGACCTTCAG-----GCAATCCT 97
D 441 LeuGlnGlyThrGlyProArgCysGluIleAspValAsnGluCysValSerAsnPro 460
QY 98 CTCAGGATGATTGGCCCAACCTTCCTGGTGTACTACGCTCAGACTCTGATCTA 157
D 461 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysMetCysMet 479
QY 158 CCA-----CAAGATGTTCCCTGT 175
D 480 ProGlyThrGluGlyValHisCysGluValAsnThrAspGluCysAlaSerSerProCys 499
QY 176 CTGGAGGTAGTAATGCTGGACATGTTACTTCTTCAAGACAAG----- 223
D 500 LeuHisAsnGlyArgCysLeuAspYsIleAsnGluPheGlnCysGluCysProThrGly 519
QY 224 -----CAGATTGCCAAGGCAAGGACCTTTCGATAGCACTGGAAGCCAGAA 274
D 520 PheThrGlyHisLeuCysGlnIleAspValAspGluCysAlaSerThr----- 535
QY 275 ATGTGCTCTGAGAACGATCTGTGTCATCTGACGGTCTGCTTTCGAGTGCCTTTGT 334
D 536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyThrCysValCys 554
QY 335 GCTGATGTTTCATGATACAAAGT-----ATGGCAGGCTCATTTCACTGCTTATGTTCTTTGG 400
D 555 ThrGluGlyThrGlyThrHisCysGluValAspIleAspGluCysAspProAspPro 574
QY 362 -----ATGGCAGGCTCATTTCACTGCTTATGTTCTTTGG 400
D 575 CysHisTyThrGlySerCysLysAspGlyValAlaThrPheThrCysLeuCysArgProG 594
QY 401 ATTC 404
D 594 ytyr 595

RESULT 8
NTC3_RAT
ID NTC3_RAT STANDARD; PRT; 2319 AA.
AC Q9R172;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurogenic locus notch homolog protein 3 precursor (Notch 3).
GN NOTCH3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RA Hartunians T., Boulter J., Weinmaster G., Schanen N.C.;
RT "Rattus norvegicus mRNA for Notch 3.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP FUNCTION.
RX MEDLINE=21094508; PubMed=11182080;
RA Tanigaki K., Nogaki F., Takanashi J., Tashiro K., Kurooka H.,
RA Honjo T.;
RT "Notch1 and Notch3 instructively restrict bFGF-responsive multipotent
RT neural progenitor cells to an astroglial fate.";
RL Neuron 29:45-55(2001).
RN [3]
RP TISSUE SPECIFICITY.
RX MEDLINE=21331789; PubMed=11438922;
RA Irvin D.K., Zurcher S.D., Nguyen T., Weinmaster G., Kornblum H.I.;
RT "Expression patterns of Notch1, Notch2, and Notch3 suggest multiple
RT functional roles for the Notch-DSL signaling system during brain
RT development.";
RL J. Comp. Neurol. 436:167-181(2001).
```

```
-!- FUNCTION: Functions as a receptor for membrane-bound ligands
Jagged1, Jagged2 and Deltal to regulate cell-fate determination.
Upon ligand activation through the released notch intracellular
domain (NICD) it forms a transcriptional activator complex with
RBP-J kappa and activates genes of the enhancer of split locus.
Affects the implementation of differentiation, proliferation and
apoptotic programs (By similarity). Acts instructively to control
the cell fate determination of CNS multipotent progenitor cells,
resulting in astroglial induction and neuron/oligodendrocyte
suppression.
-!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
terminal fragment N(EC) which are probably linked by disulfide
bonds (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein. Following
proteolytical processing NICD is translocated to the nucleus.
-!- TISSUE SPECIFICITY: Expressed in postnatal central nervous system
(CNS) germinal zones and, in early postnatal life, within
numerous cells throughout the CNS. It is more highly localized
to ventricular germinal zones.
-!- PMW: Synthesized in the endoplasmic reticulum as an inactive form
which is proteolytically cleaved by a furin-like convertase in the
trans-Golgi network before it reaches the plasma membrane to yield
an active, ligand-accessible form. Cleavage results in a C-
terminal fragment N(TM) and a N-terminal fragment N(EC). Following
ligand binding, it is cleaved by TNF-alpha converting enzyme
(TACE) to yield a membrane-associated intermediate fragment called
notch extracellular truncation (NEXT). This fragment is then
cleaved by presenilin dependent gamma-secretase to release a
notch-derived peptide containing the intracellular domain (NICD)
from the membrane (By similarity).
-!- PTM: Phosphorylated (By similarity).
-!- SIMILARITY: Belongs to the NOTCH family.
-!- SIMILARITY: Contains 34 EGF-like domains.
-!- SIMILARITY: Contains 3 Lin/Notch repeats.
-!- SIMILARITY: Contains 5 ANK repeats.
```

```
-----
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
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EMBL; AF164486; AAD46653.2; ..
HSSP; P00740; 1EDM.
InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx_hydroxyl_S.
InterPro; IPR000742; EGF_2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR006209; EGF_like.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR008297; Notch_dom.
InterPro; IPR008800; Notch_dom.
Pfam; PF00023; ank; 6.
Pfam; PF00066; notch; 3.
Pfam; PIRSF002279; Notch; 1.
PRINTS; PR00010; EGFBLD.
PRINTS; PR00011; EGFBLMININ.
PRINTS; PR01452; NOTCH.
SMART; SMO0248; ANK; 6.
SMART; SMO0179; EGF_CA; 20.
SMART; SMO0004; NL; 3.
DR PROSITE; PS50297; ANK_REPEAT; 1.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS00010; ASX_HYDROXYL; 18.
DR PROSITE; PS00022; EGF_1; 33.
DR PROSITE; PS01186; EGF_2; 26.
DR PROSITE; PS50026; EGF_3; 34.
DR PROSITE; PS01187; EGF_CA; 16.
KW Receptor; Transcription regulation; Activator; Differentiation;
```


FT	DISULFID	303	319	BY SIMILARITY.
FT	DISULFID	321	330	BY SIMILARITY.
FT	DISULFID	337	348	BY SIMILARITY.
FT	DISULFID	342	357	BY SIMILARITY.
FT	DISULFID	359	368	BY SIMILARITY.
FT	DISULFID	375	385	BY SIMILARITY.
FT	DISULFID	380	395	BY SIMILARITY.
FT	DISULFID	397	406	BY SIMILARITY.
FT	DISULFID	413	424	BY SIMILARITY.
FT	DISULFID	418	433	BY SIMILARITY.
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FT	DISULFID	531	546	BY SIMILARITY.
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FT	DISULFID	690	699	BY SIMILARITY.
FT	DISULFID	706	717	BY SIMILARITY.
FT	DISULFID	711	726	BY SIMILARITY.
FT	DISULFID	728	737	BY SIMILARITY.
FT	DISULFID	783	794	BY SIMILARITY.
FT	DISULFID	788	803	BY SIMILARITY.
FT	DISULFID	805	814	BY SIMILARITY.
FT	DISULFID	821	832	BY SIMILARITY.
FT	DISULFID	826	841	BY SIMILARITY.
FT	DISULFID	843	852	BY SIMILARITY.
FT	DOMAIN	938	941	POLY-PRO.
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	214	214	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	556	556	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	742	742	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	957	957	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	988	988	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	1042	1042	N-LINKED (GLCNAC. .) (POTENTIAL).
FS	SEQUENCE	1213	AA; 133365 MW; 5C5F16A7E20D9534	CRC64;

Alignment Scores:				
Pred. No.:	0.0314	Length:	1213	
Score:	99.00	Matches:	23	
Percent Similarity:	43.75%	Conservative:	12	
Best Local Similarity:	28.75%	Mismatches:	22	
Query Match:	11.15%	Indels:	23	
DB:	1	Gaps:	3	

US-09-773-476-294 (1-489) x JAG3_BRARE (1-1213)	
QY	224 CAGATTGCCAAGGCGAAGGACCTTTTGCATAGCACTGGAGCCGCAAGTAATGTGCTT 283
Db	288 GlnLeuCys-----AspLysAspLeu---AsnTyrCysGlyThrHisGlnProCysLeu 304
QY	284 GAGAACGGATCTGTGCATCTGACGGTCTGCTCTTTTGCAGTGGGTTTGCTGATGGT 343
Db	305 AsnGlyGlyThrCysSerAsnThrGlyProAspLysTyrGlnCysSerCysGluAspGly 324
QY	344 TTCATCGATACAAAGTGATGAGGCGAGGCTCAT----- 377
Db	325 TyrSerGlyValAsnCysGluArg-AlaGluHisAlaCysLeuSerAsnProCysAlaAs 344
QY	378 -----TTTCACTGCTTATGTTCTTTGGGATTC 404
Db	344 nGlyGlyThrCysLysGluThrSerGlnGlyThrGlyLysCysHisCysAlaIleGlyTrp 363

RESULT 10
NTC4 MOUSE

NTC4_MOUSE STANDARD; PRT; 1964 AA.
AC P11695; O35442; O88314; O88316; Q62389; Q62390; Q9RIW9; Q9RI1X0;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)
GN [Contains: Transforming protein Int-3].
GN NOTCH4 OR INT3 OR INT-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN MEDLINE=92194507; PubMed=1312643;
RP MEDLINE=92194507; PubMed=1312643;
RX Robbins J., Blondel B.J., Gallahan D., Callahan R.;
RT "Mouse mammary tumor gene int-3: a member of the notch gene family
RT transforms mammary epithelial cells.";
RL J. Virol. 66:2594-2599(1992).
RN [2]
RN REVISIONS, SEQUENCE FROM N.A.
RX MEDLINE=97294599; PubMed=9150355;
RX Gallahan D., Callahan R.;
RT "The mouse mammary tumor associated gene INT3 is a unique member of
RT the NOTCH gene family (NOTCH4).";
RL Oncogene 14:1883-1890(1997).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Lung, and Testis;
RP MEDLINE=96281668; PubMed=8681805;
RX Uytendaele H., Marazzi G., Wu G., Van Q., Sassoon D., Kitajewski J.;
RT "Notch4/int-3, a mammary proto-oncogene, is an endothelial
RT cell-specific mammalian Notch gene.";
RL Development 122:2251-2259(1996).
RN [4]
RN SEQUENCE FROM N.A.
RP Rowen L., Mahairas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
RA Loretz C., Schmidt S., Traicoff R., Zackrone K., Hood L.;
RT "Sequence of the mouse major histocompatibility locus class III
RT region.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE OF 1436-1600 FROM N.A.
RX MEDLINE=99252212; PubMed=10233982;
RA Lee J.-S., Haruna T., Ishimoto A., Honjo T., Yanagawa S.-I.;
RT "Intracisternal type A particle-mediated activation of the Notch4/int3
RT gene in a mouse mammary tumor: generation of truncated Notch4/int3
RT mRNAs by retroviral splicing events.";
RL J. Virol. 73:5166-5171(1999).
RN [6]
RN FUNCTION.
RX MEDLINE=21244657; PubMed=11344305;
RA Uytendaele H., Ho J., Rossant J., Kitajewski J.;
RT "Vascular patterning defects associated with expression of activated
RT Notch4 in embryonic endothelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).
RN [7]
RN SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS
OF VAL-1463.
RX MEDLINE=21523956; PubMed=11518718;
RA Saxena M.I., Schroeter E.H., Mumm J.S., Kopan R.;
RT "Murine notch homologs (N1-4) undergo presenilin-dependent
RT proteolysis.";
RL J. Biol. Chem. 276:40268-40273(2001).
RN [8]
RN POST-TRANSLATIONAL PROCESSING.
RX MEDLINE=21374376; PubMed=11459941;
RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
RT "Conservation of the biochemical mechanisms of signal transduction
RT among mammalian Notch family members.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands
Jagged1, Jagged2 and Delta to regulate cell-fate determination.

CC Upon ligand activation through the released notch intracellular
CC domain (NICD) it forms a transcriptional activator complex with
CC RBP-J kappa and activates genes of the enhancer of split locus.
CC Affects the implementation of differentiation, proliferation and
CC apoptotic programs (By similarity). May regulate branching
CC morphogenesis in the developing vascular system.
CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
CC terminal fragment N(EC) which are probably linked by disulfide
CC bonds.
CC -!- CELLULAR LOCATION: Type I membrane protein. Following
CC proteolytical processing NICD is translocated to the nucleus.
CC -!- TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart
CC kidney, and at lower levels in the ovary and skeletal muscle. A
CC very low expression is seen in the brain, intestine, liver and
CC testis.
CC -!- DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during
CC embryonic development from 9.0 dpc.
CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form
CC which is proteolytically cleaved by a furin-like convertase in the
CC trans-Golgi network before it reaches the plasma membrane to yield
CC an active, ligand-accessible form. Cleavage results in a C-
CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
CC ligand binding, it is cleaved by TNF-alpha converting enzyme
CC (TACE) to yield a membrane-associated intermediate fragment called
CC notch extracellular truncation (NEXT). This fragment is then
CC cleaved by presenilin dependent gamma-secretase to release a
CC notch-derived peptide containing the intracellular domain (NICD)
CC from the membrane.
CC -!- PTM: Phosphorylated.
CC -!- DISEASE: Loss of the extracellular domain causes constitutive
CC activation of the Notch protein, which leads to hyperproliferation
CC of glandular epithelial tissues and development of mammary
CC carcinomas.
CC -!- SIMILARITY: Belongs to the NOTCH family.
CC -!- SIMILARITY: Contains 29 EGF-like domains.
CC -!- SIMILARITY: Contains 3 Lin/Notch repeats.
CC -!- SIMILARITY: Contains 5 ANK repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)
CC or send an email to license@isb-sib.ch.
CC -----
CC EMBL; M80456; AAB39377.1; -.
CC EMBL; U43691; AAC52630.1; -.
CC EMBL; U43691; AAC52631.1; -.
CC EMBL; AF030001; AAB82004.1; -.
CC EMBL; AB016771; BAA32281.1; ALT SEQ.
CC EMBL; AB016772; BAA32283.1; ALT_INIT.
CC EMBL; AB016773; BAA32284.1; ALT_INIT.
CC EMBL; AB016774; BAA32285.1; -.
CC PIR; A38072; TVMVT3.
CC PIR; T09059; T09059.
CC HSSP; P08709; 1BF9.
CC MGP; MGI:107471; Notch4.
CC InterPro; IPR002110; ANK.
CC InterPro; IPR000152; Asx_hydroxyl_S.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR001881; EGF_Ca.
CC InterPro; IPR001438; EGF_II.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR008297; Notch.
CC InterPro; IPR008800; Notch_dom.
CC Pfam; PF00023; ank; 6.
CC Pfam; PF00008; EGF; 27.
CC Pfam; PF00066; notch; 2.
CC PIRSF; PIRSF002279; Notch; 1.
CC PRINTS; PR00010; EGFLOOD.
CC PRINTS; PR00011; EGFLAMININ.

DR PRINTS; PRO1452; NOTCH.
DR SMART; SMO0248; ANK; 6.
DR SMART; SMO0179; EGF_CA; 11.
DR SMART; SMO0004; NL; 2.
DR PROSITE; PS00297; ANK REP REGION; 1.
DR PROSITE; PS00088; ANK REPEAT; 5.
DR PROSITE; PS00010; ASX-HYDROXYL; 11.
DR PROSITE; PS00022; EGF_1; 28.
DR PROSITE; PS01186; EGF_2; 21.
DR PROSITE; PS00026; EGF_3; 27.
DR PROSITE; PS01187; EGF_CA; 9.
KW Receptor; Transcription regulation; Activator; Differentiation;
KW Developmental protein; Repeat; ANK repeat; EGF-like domain;
KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Proto-oncogene.
FT SIGNAL 1 20
FT CHAIN 21 1964
FT CHAIN 1411 1964
FT CHAIN 1428 1964
FT CHAIN 1463 1964
FT DOMAIN 21 1443
FT DOMAIN 1444 1464
FT TRANSMEM 1444 1464
FT DOMAIN 1465 1964
FT DOMAIN 21 60
FT DOMAIN 61 112
FT DOMAIN 115 152
FT DOMAIN 153 189
FT DOMAIN 191 229
FT DOMAIN 231 271
FT DOMAIN 273 309
FT DOMAIN 311 350
FT DOMAIN 352 388
FT DOMAIN 389 427
FT DOMAIN 429 470
FT DOMAIN 472 508
FT DOMAIN 510 546
FT DOMAIN 548 594
FT DOMAIN 596 632
FT DOMAIN 633 656
FT DOMAIN 658 686
FT DOMAIN 688 724
FT DOMAIN 726 762
FT DOMAIN 764 800
FT DOMAIN 803 839
FT DOMAIN 841 877
FT DOMAIN 878 924
FT DOMAIN 926 962
FT DOMAIN 964 1000
FT DOMAIN 1002 1040
FT DOMAIN 1042 1081
FT DOMAIN 1083 1122
FT DOMAIN 1126 1167
FT REPEAT 1168 1208
FT REPEAT 1209 1242
FT REPEAT 1243 1282

Alignment Scores:
Pred. No.: 0.0345 Length: 1964
Score: 99.00 Matches: 37
Percent Similarity: 34.87% Conservative: 16
Best Local Similarity: 24.34% Mismatches: 52
Query Match: 11.15% Indels: 47
DB: 1 Gaps: 8

US-09-773-476-294 (1-489) x NTC4_MOUSE (1-1964)
QY 41 GGTCACAACTTT-----TTACAGGCTTATCTGCTATTATCATACCTTCAG 88
Db 860 GlyProSerPheGlnCysLeuCysLeuGlnGlyTrpThrGlyAlaLeuCysAspPhe--- 878
QY 89 GCAAAATCTCTCAAGATGATTGGCCACACCTCCGGTGGTACTCAGCTGCAGACT 148
Db 879 -----ProLeuSerCysGlnMetAlaMetSerGlnGlyLe-----GluileSerGly 895

QY 149 CTGATACCTACCACAGATGTTCCCTGCTGGAGGTAGTAATGCTGGGACATGTTACT 208
Db 896 Leu-----CysGlnAsnGlyGlyLeuCysIleAspThrGlySer 908
QY 209 TCTTTCAAGGACAAAG-----CAGATTTCACCAAGGGCAAGGGAC 247
Db 909 SerTy-PheCysArgCysProGlyPheGlnGlyLysLeuCysGlnAspAsnMetAsn 928
QY 248 CTTTGCAATAGCACTGGAGGCCAGAAATGTCTCTGAGACGGATCTTGTCATCTGAC 307
Db 929 ProCys-----GluProAsnProCysHisHisGlySerThrCysValProGln 944
QY 308 GGTCCCTGGTCTTTGTCAGTCGCGTTTGTGTGATGGTTTCATGGATACCAAGTG----- 361
Db 945 ProSerGlyTyVal---CysGlnCysAlaProGlyTyTrGluGlyGlnAsnCysSerLys 963
QY 362 -----ATGAGGCAG 370
Db 964 ValLeuGluAlaCysGlnSerGlnProCysHisAsnHisGlyThrCysThrSerArgPro 983
QY 371 GGTCATTTTCACTGCTTATGTTCTTTGGGATTC 404
Db 984 GlyGly-PheHisCysAlaCysProGlyPhe 994
RESULT 11
NTC4 HUMAN STANDARD; PRT; 2003 AA.
ID AC Q99456; Q0306; Q99458; Q99940; Q9H3S8; Q9UII9; Q9UIJ0;
DC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)
GN NOTCH4.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU.
RC TISSUE=Placenta;
RX MEDLINE=97311416; PubMed=9168133;
RA Sugaya K., Sasanuma S.-I., Nohata J., Kimura T., Fukagawa T.,
RA Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.;
RT "Gene organization of human NOTCH4 and (CTG)n polymorphism in this
human counterpart gene of mouse proto-oncogene Int3.";
RL Gene 189:235-244(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Bone marrow, and Heart;
RX MEDLINE=98360091; PubMed=9693032;
RA Li L., Huang G.M., Banta A.B., Deng Y., Smith T., Dong P.,
RA Friedman C., Chen L., Trask B.J., Spies T., Rowen L., Hood L.;
RT "Cloning, characterization, and the complete 56.8-kilobase DNA
sequence of the human NOTCH4 gene.";
RL Genomics 51:45-58(1998).
RN [3]
RP SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317.
RX MEDLINE=99180765; PubMed=10079256;
RA Miyagawa T., Tokunaga K., Hojho H.;
RT "Human notch4 gene variant.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP IDENTIFICATION OF LIGANDS.
RX MEDLINE=99180765; PubMed=10079256;
RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L., S.;
RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Teakonas S.;
RT "Human ligands of the Notch receptor.";
RL Am. J. Pathol. 154:785-794(1999).
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands
CC Jagged1, Jagged2 and Delta1 to regulate cell fate determination.
CC Upon ligand activation through the released notch intracellular
CC domain (NICD) it forms a transcriptional activator complex with
CC RBP-J kappa and activates genes of the enhancer of split locus.

CC Affects the implementation of differentiation, proliferation and
 CC apoptotic programs. May regulate branching morphogenesis in the
 CC developing vascular system (By similarity).
 CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
 CC terminal fragment N(EC) which are probably linked by disulfide
 CC bonds (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Comment=Experimental confirmation may be lacking for some
 CC isoforms;
 CC Name=1;
 CC IsoId=Q99466-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q99466-2; Sequence=VSP_001406;
 CC Name=3;
 CC IsoId=Q99466-3; Sequence=VSP_001407;
 CC -!- TISSUE SPECIFICITY: Highly expressed in the heart, moderately in
 CC the lung and placenta and at low levels in the liver, skeletal
 CC muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow
 CC and fetal liver. No expression was seen in adult brain or
 CC peripheral blood leukocytes.
 CC -!- PMW: Synthesized in the endoplasmic reticulum as an inactive form
 CC which is proteolytically cleaved by a furin-like convertase in the
 CC trans-Golgi network before it reaches the plasma membrane to yield
 CC an active, ligand-accessible form. Cleavage results in a C-
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (NEXT). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane (By similarity).
 CC -!- PMW: Phosphorylated (By similarity).
 CC -!- POLYPEPTIDE: The poly-Leu region of NOTCH4 (in the signal
 CC peptide) is polymorphic and the number of Leu varies in the
 CC population (from 6 to 12).
 CC -!- SIMILARITY: Belongs to the NOTCH family.
 CC -!- SIMILARITY: Contains 28 EGF-like domains.
 CC -!- SIMILARITY: Contains 3 lin/Notch repeats.
 CC -!- SIMILARITY: Contains 5 ANK repeats.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
 CC in position 1438 to 1463.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; D63395; BAA09708.1; ALT_FRAME.
 CC EMBL; D85566; BAA13116.1; -.
 CC EMBL; U95299; AAC32288.1; -.
 CC EMBL; U95335; AAC63097.1; -.
 CC EMBL; AB023961; BAB20317.1; -.
 CC EMBL; AB024520; BAA88951.1; -.
 CC EMBL; AB024578; BAA88952.1; -.
 CC HSP; P08709; IBF9.
 CC Genew; HGNC:7884; NOTCH4.
 CC MIM; 164951; -.
 CC InterPro; IPR002110; ANK.
 CC InterPro; IPR000152; Asx_hydroxyl_S.
 CC InterPro; IPR000742; EGF_2.
 CC InterPro; IPR001881; EGF_Ca.
 CC InterPro; IPR001438; EGF_II.
 CC InterPro; IPR006209; EGF_Like.
 CC InterPro; IPR002049; Laminin_EGF.
 CC InterPro; IPR008297; Notch.
 CC InterPro; IPR008000; Notch_dom.
 CC Pfam; PF00023; ank; 6.

DR Pfam; PF00008; EGF; 26.
 DR Pfam; PF00066; notch; 2.
 DR PIRSF; PIRSF002279; Notch; 1.
 DR PRINTS; PR00010; EGFBL00D.
 DR PRINTS; PR00011; EGFAMININ.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SMART0248; ANK; 5.
 DR SMART; SMART0179; EGF_CA; 11.
 DR SMART; SMART0004; NL; 3.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS50088; ANK_REPEAT; 5.
 DR PROSITE; PS00010; ASX_HYDROXYL; 11.
 DR PROSITE; PS00022; EGF_1; 28.
 DR PROSITE; PS01186; EGF_2; 21.
 DR PROSITE; PS50026; EGF_3; 28.
 DR PROSITE; PS01187; EGF_CA; 9.
 KW Receptor; Transcription regulation; Activator; Differentiation;
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;
 KW Triplet repeat expansion; Alternative splicing.
 FT SIGNAL 1 23
 FT CHAIN 24 2003
 FT CHAIN 1432 2003
 FT CHAIN 1467 2003
 FT DOMAIN 24 1447
 FT TRANSMEM 1448 1468
 FT DOMAIN 1469 2003
 FT DOMAIN 24 63
 FT DOMAIN 64 115
 FT DOMAIN 118 155
 FT DOMAIN 156 192
 FT DOMAIN 194 232
 FT DOMAIN 234 274
 FT DOMAIN 276 312
 FT DOMAIN 314 353
 FT DOMAIN 355 391
 FT DOMAIN 392 430
 FT DOMAIN 432 473
 FT DOMAIN 475 511
 FT DOMAIN 513 549
 FT DOMAIN 551 587
 FT DOMAIN 589 625
 FT DOMAIN 626 659
 FT DOMAIN 661 689
 FT DOMAIN 691 727
 FT DOMAIN 729 765
 FT DOMAIN 767 803
 FT DOMAIN 806 842
 FT DOMAIN 844 880
 FT DOMAIN 882 928
 FT DOMAIN 930 966
 FT DOMAIN 968 1004
 FT DOMAIN 1006 1044
 FT DOMAIN 1046 1085
 FT DOMAIN 1087 1126
 FT DOMAIN 1130 1171
 FT DOMAIN 1172 1212
 FT REPEAT 1165 1212
 FT REPEAT 1213 1246
 FT REPEAT 1247 1286
 FT REPEAT 1633 1665
 FT REPEAT 1666 1698
 FT REPEAT 1700 1732
 FT REPEAT 1733 1765
 FT REPEAT 1766 1798
 FT DISULFID 28 41
 FT DISULFID 35 51
 FT DISULFID 53 62
 FT DISULFID 68 80
 FT DISULFID 74 103
 FT DISULFID 105 114
 POTENTIAL.
 NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG 4.
 NOTCH EXTRACELLULAR TRUNCATION
 (BY SIMILARITY).
 NOTCH INTRACELLULAR DOMAIN
 (BY SIMILARITY).
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 EGF-LIKE 1.
 EGF-LIKE 2.
 EGF-LIKE 3.
 EGF-LIKE 4.
 EGF-LIKE 5.
 EGF-LIKE 6.
 EGF-LIKE 7.
 EGF-LIKE 8.
 EGF-LIKE 9.
 EGF-LIKE 10.
 EGF-LIKE 11.
 EGF-LIKE 12.
 EGF-LIKE 13.
 EGF-LIKE 14.
 EGF-LIKE 15.
 EGF-LIKE 16.
 EGF-LIKE 17.
 EGF-LIKE 18.
 EGF-LIKE 19.
 EGF-LIKE 20.
 EGF-LIKE 21.
 EGF-LIKE 22.
 EGF-LIKE 23.
 EGF-LIKE 24.
 EGF-LIKE 25.
 EGF-LIKE 26.
 EGF-LIKE 27.
 EGF-LIKE 28.
 EGF-LIKE 29.
 POLY-ARG.
 LIN/NOTCH 1.
 LIN/NOTCH 2.
 LIN/NOTCH 3.
 ANK 1.
 ANK 2.
 ANK 3.
 ANK 4.
 ANK 5.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.
 BY SIMILARITY.

FT	DISULFID	122	133	BY SIMILARITY.
FT	DISULFID	127	143	BY SIMILARITY.
FT	DISULFID	145	154	BY SIMILARITY.
FT	DISULFID	160	171	BY SIMILARITY.
FT	DISULFID	165	180	BY SIMILARITY.
FT	DISULFID	182	191	BY SIMILARITY.
FT	DISULFID	198	211	BY SIMILARITY.
Alignment Scores:				
Pred. No.:	0.0347	Length:	2003	
Score:	99.00	Matches:	32	
Percent Similarity:	37.7%	Conservative:	8	
Best Local Similarity:	30.1%	Mismatches:	34	
Query Match:	11.1%	Indels:	32	
DB:	1	Gaps:	6	
US-09-773-476-294 (1-489) x NTC4_HUMAN (1-2003)				
QY	107	GATTGGCCACACTTCCTGGTGGTTACTAGTCGACACTCTGATACCTACCA	-----	160
DB	530	AspLeuLeuAsnGlyPhe		
QY	161	-----CAAGATGTT		
DB	544	SerGlyThrArgCysGluGluAspLeuSerProCysAlaAsnGly		
QY	185	AGTAATGCTGGACAACTTCTCTTCAAGGCAAGCAGATT	-----	229
DB	564	GlyGlnCysGlnProGlyAlaPheHscysLysCysLeuProGlyPheGluGly		
QY	230	-----TGCCAGGGCAAGGACCTTTCATAGCAGCTGGAAGCCAGAAATGTCCT	283	
DB	584	ProArgCysGlnThrGluValAspGluCysLeuSer		
QY	284	GAGAACGGATCTGTCATCTGACGCTCTGCTGCTTTTCAGTGGGTTTGCTGATGT	343	
DB	600	ValGlyAlaSerCysLeu---AspLeuProGlyAlaPhePheCysLeuCysProSerGly	618	
QY	344	TTCCATGGATACAAAGTGT	361	
DB	619	PheThrGlyGlnLeuCys	624	

RESULT 12
LTBS_MOUSE
ID LTBS_MOUSE STANDARD; PRT; 1389 AA.
AC Q8CG18; Q8CNW7; Q8C7F5; Q8C1R0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Latent transforming growth factor beta binding protein, isoform 1S
DE precursor (LTBP-1) (Transforming growth factor beta-1 binding protein
DE 1) (TGF-beta1-BP-1).
GN LTBP1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22597538; PubMed=12711388;
RA Noguera I., Obata H., Gualandris A., Cowin P., Rifkin D.B.;
RT "Molecular cloning of the mouse Ltbp-1 gene reveals tissue specific
RT expression of alternatively spliced forms.";
RL Gene 308.31-41(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SVJ;
RA Weiskirchen R., Moser M., Guenther K., Weiskirchen S., Gressner A.M.;
RT "The murine latent transforming growth factor-beta binding protein
RT (ltbp-1) is alternatively spliced, and maps to a region syntenic to
RT human chromosome 2p21-22.";
RL Gene 308.43-52(2003).

[3]
RN SEQUENCE OF 788-1389 FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Aorta, Liver, and Vein;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nkaido I., Osato N., Saito K., Suzuki H., Yananaka I., Kiyosawa H.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Brad D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- SUBUNIT: The large latent complex of TGF-beta1 from platelets is
CC composed of the TGF-beta1 molecule noncovalently associated with a
CC disulfide-bonded complex of a dimer of the N-terminal propeptide
CC of the TGF-beta1 precursor and a third component denoted TGF-
CC beta1-BP. TGF-beta1-BP does not bind directly to active TGF-BETA1.
CC Binds to fibrillin (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1S;
CC IsoId=Q8CG18-1; Sequence=Displayed;
CC Name=1L;
CC IsoId=Q8CG19-1; Sequence=External;
CC -!- PTM: Contains hydroxylated asparagine residues (By similarity).
CC -!- PTM: The N-terminus is blocked (By similarity).
CC -!- SIMILARITY: Contains 16 EGF-like domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF346455; AAN77251.1;
DR EMBL; AF346438; AAN77251.1; JOINED.
DR EMBL; AF346439; AAN77251.1; JOINED.
DR EMBL; AF346440; AAN77251.1; JOINED.
DR EMBL; AF346441; AAN77251.1; JOINED.
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DR EMBL; AF346443; AAN77251.1; JOINED.
DR EMBL; AF346444; AAN77251.1; JOINED.
DR EMBL; AF346445; AAN77251.1; JOINED.
DR EMBL; AF346446; AAN77251.1; JOINED.
DR EMBL; AF346447; AAN77251.1; JOINED.
DR EMBL; AF346448; AAN77251.1; JOINED.
DR EMBL; AF346449; AAN77251.1; JOINED.
DR EMBL; AF346450; AAN77251.1; JOINED.
DR EMBL; AF346451; AAN77251.1; JOINED.

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DR EMBL; AF346456; AAN77251.1; JOINED.
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DR EMBL; AF346459; AAN77251.1; JOINED.
DR EMBL; AF346460; AAN77251.1; JOINED.
DR EMBL; AF346461; AAN77251.1; JOINED.
DR EMBL; AF346462; AAN77251.1; JOINED.
DR EMBL; AF346463; AAN77251.1; JOINED.
DR EMBL; AF346464; AAN77251.1; JOINED.
DR EMBL; AY143161; AAN38831.1; JOINED.
DR EMBL; AK080024; BAC34222.1; -.
DR EMBL; AK080024; BAC37808.1; -.
DR MGD; MGI:109151; Ltbp1.
DR GO; GO:0005578; C:extracellular matrix; IDA.
DR InterPro; IPR000152; Asx_Hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002212; Fibril-assoc.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF; 15.
DR Pfam; PF00683; TB; 4.
DR SMART; SM00181; EGF; 17.
DR SMART; SM00179; EGF_Ca; 16.
DR PROSITE; PS00010; ASX HYDROXYL; 13.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 11.
DR PROSITE; PS50028; EGF_3; 13.
DR PROSITE; PS01187; EGF_CA; 15.
DR Growth factor binding; Repeat; EGF-like domain;
KW Hydroxylation; Signal; Glycoprotein;
KW Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 1389
FT DOMAIN 295 335
FT REPEAT 343 408
FT DOMAIN 542 583
FT DOMAIN 584 625
FT DOMAIN 626 666
FT DOMAIN 667 706
FT DOMAIN 707 747
FT DOMAIN 748 788
FT DOMAIN 789 829
FT DOMAIN 830 870
FT DOMAIN 871 912
FT DOMAIN 913 954
FT DOMAIN 955 997
FT REPEAT 1012 1079
FT DOMAIN 1092 1134
FT DOMAIN 1135 1175
FT REPEAT 1185 1257
FT DOMAIN 1289 1330
FT DOMAIN 1330 1374
FT DISULFID 299 310
DR EMBL; AF346452; AAN77251.1; JOINED.
DR EMBL; AF346453; AAN77251.1; JOINED.
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DR EMBL; AF346455; AAN77251.1; JOINED.
DR EMBL; AF346456; AAN77251.1; JOINED.
DR EMBL; AF346457; AAN77251.1; JOINED.
DR EMBL; AF346458; AAN77251.1; JOINED.
DR EMBL; AF346459; AAN77251.1; JOINED.
DR EMBL; AF346460; AAN77251.1; JOINED.
DR EMBL; AF346461; AAN77251.1; JOINED.
DR EMBL; AF346462; AAN77251.1; JOINED.
DR EMBL; AF346463; AAN77251.1; JOINED.
DR EMBL; AF346464; AAN77251.1; JOINED.
DR EMBL; AY143161; AAN38831.1; JOINED.
DR EMBL; AK080024; BAC34222.1; -.
DR EMBL; AK080024; BAC37808.1; -.
DR MGD; MGI:109151; Ltbp1.
DR GO; GO:0005578; C:extracellular matrix; IDA.
DR InterPro; IPR000152; Asx_Hydroxyl_S.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002212; Fibril-assoc.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF; 15.
DR Pfam; PF00683; TB; 4.
DR SMART; SM00181; EGF; 17.
DR SMART; SM00179; EGF_Ca; 16.
DR PROSITE; PS00010; ASX HYDROXYL; 13.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 11.
DR PROSITE; PS50028; EGF_3; 13.
DR PROSITE; PS01187; EGF_CA; 15.
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KW Hydroxylation; Signal; Glycoprotein;
KW Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 1389
FT DOMAIN 295 335
FT REPEAT 343 408
FT DOMAIN 542 583
FT DOMAIN 584 625
FT DOMAIN 626 666
FT DOMAIN 667 706
FT DOMAIN 707 747
FT DOMAIN 748 788
FT DOMAIN 789 829
FT DOMAIN 830 870
FT DOMAIN 871 912
FT DOMAIN 913 954
FT DOMAIN 955 997
FT REPEAT 1012 1079
FT DOMAIN 1092 1134
FT DOMAIN 1135 1175
FT REPEAT 1185 1257
FT DOMAIN 1289 1330
FT DOMAIN 1330 1374
FT DISULFID 299 310

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Alignment Scores:

Pred. No.: 0.0364
 Score: 98.50
 Percent Similarity: 34.58%
 Best Local Similarity: 28.04%
 Query Match: 11.09%
 DB: 1
 Gaps: 4

US-09-773-476-294 (1-489) x LTBS_MOUSE (1-1389)

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QY 164 GATGTCCTCTGCTGGAGGTAGTAATGCTGGGACAACTGTTCTTTCACAGCAAG 223
Db 854 AspCysThrCysProAspGlyPheGlnLeuAsnAspAsn----- 866
QY 224 CAGATTTCGCAAGGCAAGGACCTTTGCAATAGCAGCTGGAAGCCAGAAATGTGCTCT 283
Db 867 -----LysGlyCysGlnAspLe-----AsnGluCysAlaGlnProGlyLeuCysGly 882
QY 284 GAGAACGATCTTGTGATCTGACGCTGCTGCTTTTTCAGTCGCTGTTGCTGATGGT 343
Db 883 SerHisGlyGluCysLeuAsnThr---GlnGlySerPheHisCysValCysGluGlnGly 901
QY 344 TTC----- 346
Db 902 PheSerIleSerAlaAspGlyArgThrCysGluAspIleAspGluCysValAsnAsnThr 921
QY 347 -----CATGATACAACTGTATGAGGAGGCTCATTTTCACCTATGTTTC 394
Db 922 ValCysAspSerHisGlyPheCysAspAsnThrAlaGlySer-PheArgCysLeuCysTy 941
QY 395 TTTGGATCTGGGATCCA 413
Db 941 rGlnGlyPheGlnAlaPro 947

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RESULT 13

ID LTBL RAT STANDARD; PRT; 1712 AA.
 AC Q00918;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DE Latent transforming growth factor beta binding protein 1 precursor
 DE (LTBP-1) (Transforming growth factor beta-1 binding protein 1) (TGF-
 DE betaf-BP-1) (Transforming growth factor beta-1 masking protein, large
 DE subunit).
 CN LTBP1.
 OS Rattus norvegicus (Rat).


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DR EMBL; AY143161; AAN38831.1; ALT_SEQ.
DR EMBL; AK050380; BAC34222.1; -.
DR EMBL; AK080024; BAC37808.1; -.
DR HSSP; P08709; 1BP9.
DR MGD; MGI:109151; Ltbp1.
DR GO; GO:0005578; C:extracellular matrix; IDA.
DR InterPro; IPR000152; Asx hydroxyl_S.
DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002212; Fibrin-assoc.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF; 16.
DR Pfam; PF00683; TB; 4.
DR SMART; SM00181; EGF; 18.
DR SMART; SM00179; EGF_CA; 16.
DR PROSITE; PS00010; ASX HYDROXYL; 13.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 11.
DR PROSITE; PS00026; EGF_3; 14.
DR PROSITE; PS01187; EGF_CA; 15.
DR Growth factor binding; Repeat; EGF-like domain;
KW Hydroxylation; Signal; Glycoprotein;
KW Alternative splicing.
FT SIGNAL 1 23
FT CHAIN 24 1713
FT DOMAIN 619 659
FT REPEAT 667 732
FT DOMAIN 866 907
FT DOMAIN 908 949
FT DOMAIN 950 990
FT DOMAIN 991 1030
FT DOMAIN 1031 1071
FT DOMAIN 1072 1112
FT DOMAIN 1113 1153
FT DOMAIN 1154 1194
FT DOMAIN 1195 1236
FT DOMAIN 1237 1278
FT DOMAIN 1279 1321
FT REPEAT 1336 1403
FT DOMAIN 1416 1458
FT DOMAIN 1459 1499
FT REPEAT 1509 1591
FT DOMAIN 1613 1653
FT DOMAIN 1654 1698
FT DISULFID 623 634
FT DISULFID 629 643
FT DISULFID 645 658
FT DISULFID 870 882
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FT DISULFID 893 906
FT DISULFID 912 924
FT DISULFID 919 933
FT DISULFID 935 948
FT DISULFID 954 965
FT DISULFID 960 974
FT DISULFID 977 989
FT DISULFID 995 1006
FT DISULFID 1001 1035
FT DISULFID 1018 1029
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FT DISULFID 1041 1055
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FT DISULFID 1076 1087
FT DISULFID 1082 1096
FT DISULFID 1098 1111
FT DISULFID 1117 1128
FT DISULFID 1123 1137
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DR EMBL; AK080024; BAC37808.1; -.
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DR InterPro; IPR001881; EGF_CA.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002212; Fibrin-assoc.
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF; 16.
DR Pfam; PF00683; TB; 4.
DR SMART; SM00181; EGF; 18.
DR SMART; SM00179; EGF_CA; 16.
DR PROSITE; PS00010; ASX HYDROXYL; 13.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 11.
DR PROSITE; PS00026; EGF_3; 14.
DR PROSITE; PS01187; EGF_CA; 15.
DR Growth factor binding; Repeat; EGF-like domain;
KW Hydroxylation; Signal; Glycoprotein;
KW Alternative splicing.
FT SIGNAL 1 23
FT CHAIN 24 1713
FT DOMAIN 619 659
FT REPEAT 667 732
FT DOMAIN 866 907
FT DOMAIN 908 949
FT DOMAIN 950 990
FT DOMAIN 991 1030
FT DOMAIN 1031 1071
FT DOMAIN 1072 1112
FT DOMAIN 1113 1153
FT DOMAIN 1154 1194
FT DOMAIN 1195 1236
FT DOMAIN 1237 1278
FT DOMAIN 1279 1321
FT REPEAT 1336 1403
FT DOMAIN 1416 1458
FT DOMAIN 1459 1499
FT REPEAT 1509 1591
FT DOMAIN 1613 1653
FT DOMAIN 1654 1698
FT DISULFID 623 634
FT DISULFID 629 643
FT DISULFID 645 658
FT DISULFID 870 882
FT DISULFID 877 891
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FT DISULFID 912 924
FT DISULFID 919 933
FT DISULFID 935 948
FT DISULFID 954 965
FT DISULFID 960 974
FT DISULFID 977 989
FT DISULFID 995 1006
FT DISULFID 1001 1035
FT DISULFID 1018 1029
FT DISULFID 1035 1046
FT DISULFID 1041 1055
FT DISULFID 1057 1070
FT DISULFID 1076 1087
FT DISULFID 1082 1096
FT DISULFID 1098 1111
FT DISULFID 1117 1128
FT DISULFID 1123 1137
FT DISULFID 1139 1152
FT DISULFID 1158 1170
FT DISULFID 1165 1179
FT DISULFID 1181 1193
FT DISULFID 1199 1211
FT DISULFID 1205 1220 POTENTIAL.
FT DISULFID 1222 1235 POTENTIAL.
FT DISULFID 1241 1253 POTENTIAL.
FT DISULFID 1247 1262 POTENTIAL.
FT DISULFID 1264 1277 POTENTIAL.
FT DISULFID 1283 1295 POTENTIAL.
FT DISULFID 1290 1304 POTENTIAL.
Alignment Scores:
Pred. No.: 0.038 Length: 1713
Score: 98.50 Matches: 30
Percent Similarity: 34.58% Conservative: 7
Best Local Similarity: 28.04% Mismatches: 34
Query Match: 11.09% Indels: 36
DB: 1 Gaps: 4
US-09-773-476-294 (1-489) x LTBL_MOUSE (1-1713)
Qy 164 GATGTTCCCTGCTGAGGAGTAGTAGCTGGAGCAATGTTACTTCTTCAAGGACAAG 223
Db 1178 AspCysThrCysProAspGlyPheGlnLeuAsnAspAsn----- 1190
Qy 224 CAGATTTGCCAAGGGCAAGGACCTTTGCAATAGCAGCTGAAAGCCAGAAATGTGTCT 283
Db 1191 -----LysGlyCysGlnAspIle---AsnGluCysAlaGlnProGlyLeuCysGly 1206
Qy 284 GAGAACGATCTTGTGCATCTGACGCTCGTGGTCTTTTGCAGTGCCTTGTCTGATGCT 343
Db 1207 SerHisGlyGluCysLeuAsnThr---GlnGlySerPheHisCysValCysGluGlnGly 1225
Qy 344 TTC----- 346
Db 1226 PheSerIleSerAlaAspGlyArgThrCysGluAspIleAspGluCysValAsnAsnThr 1245
Qy 347 -----CATGGATACAAAGTAGTATGAGGACGAGGCTCATTTTACGCTGATGCTTC 394
Db 1246 ValCysAspSerHisGlyPheCysAspAsnThrAlaGlySer-PheArgCysLeuCys 1265
Qy 395 TTGGGATTTGGGATCCA 413
Db 1265 rGlnGlyPheGlnAlaPro 1271
RESULT 15
NTC3 HUMAN STANDARD; PRT; 2321 AA.
ID Q9UN47; Q9UBB3; Q9UPL3; Q9Y6L8;
AC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neurogenic locus notch homolog protein 3 precursor (Notch 3).
GN NOTCH3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97032728; PubMed=8878478;
RA Joutel A., Corpechot C., Ducros A., Vahedi K., Chabrier H., Mouton P.,
RA Alamowitch S., Domenga V., Cecillon M., Marechal E., Maciazek J.,
RA Vaysiere C., Cruaud C., Cabanis E.-A., Ruchoux M.M., Weissenbach J.,
RA Bach J.-F., Bousser M.-G., Tournier-Lasserre E.;
RT "Notch3 mutations in CADASIL, a hereditary adult-onset condition
RT causing stroke and dementia.";
RL Nature 383:707-710 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX Gunel M., Artavanis-Tsakonas S.;
RA Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
```

Phan H., Velasco N., Ganes J., Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T., Trankeim M., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B., Arellano A., Olsen A.S., Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Carrano A.V., "Sequence analysis of an 1.5 Mb olfactory receptor (OLFR) cluster in 19p13.1.", Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

RA VARIANTS CADASIL TFR-49; CYS-71; CYS-90; CYS-110; CYS-133; CYS-141; ARG-146; CYS-153; CYS-169; CYS-171; CYS-182; ARG-185; SER-212; GLY-222; TYR-224; CYS-242; TYR-542; CYS-558; CYS-578; CYS-728; CYS-985; CYS-1006; CYS-1031; CYS-1031 AND ARG-1261, AND VARIANTS ARG-170; LEU-496; GLN-1133; MET-1183 AND ALA-2223.

RX MEDLINE=98049753; PubMed=9388399;

RA Joutel A., Vahedi K., Corpechot C., Troesch A., Chabrier H., Vayssiere C., Cruaud C., Maciazek J., Weissbach J., Bousser M.-G., Bach J.-F., Tournier-Lasserre E.; "Strong clustering and stereotyped nature of Notch3 mutations in CADASIL patients.", Lancet 350:1511-1515(1997).

RA [5]

RX VARIANT CADASIL 114-GLY-PRO-120 DEL. MEDLINE=20264473; PubMed=10802807;

RA Joutel A., Chabrier H., Vahedi K., Domenga V., Vayssiere C., Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserre E.; "Splice site mutation causing a seven amino acid Notch3 in-frame deletion in CADASIL.", Neurology 54:1874-1875(2000).

RA [6]

RP IDENTIFICATION OF LIGANDS.

RX MEDLINE=99180765; PubMed=10079256; Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L., Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.; "Human ligands of the Notch receptor.", Am. J. Pathol. 154:785-794(1999).

CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta1 to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity).

CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(BC) which are probably linked by disulfide bonds (By similarity).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus.

CC -1- TISSUE SPECIFICITY: Ubiquitously expressed in fetal and adult tissues.

CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(BC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).

CC -1- PTM: Phosphorylated (By similarity).

CC -1- DISEASE: Defects in NOTCH3 are associated with cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL) [MIM:123310]. CADASIL causes a type of stroke and dementia of which key features include recurrent subcortical ischemic events and vascular dementia.

CC -1- SIMILARITY: Belongs to the NOTCH family.

CC -1- SIMILARITY: Contains 34 EGF-like domains.

CC -1- SIMILARITY: Contains 3 lin/Notch repeats.

CC -1- SIMILARITY: Contains 5 ANK repeats.

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CC EMBL; U97669; RAB91371.1; --

DR EMBL; AF058900; AAC14346.1; --

DR EMBL; AF058881; AAC14346.1; JOINED.

DR EMBL; AF058882; AAC14346.1; JOINED.

DR EMBL; AF058883; AAC14346.1; JOINED.

DR EMBL; AF058884; AAC14346.1; JOINED.

DR EMBL; AF058885; AAC14346.1; JOINED.

DR EMBL; AF058886; AAC14346.1; JOINED.

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DR EMBL; AF058888; AAC14346.1; JOINED.

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DR EMBL; AF058896; AAC14346.1; JOINED.

DR EMBL; AF058897; AAC14346.1; JOINED.

DR EMBL; AF058898; AAC14346.1; JOINED.

DR EMBL; AF058899; AAC14346.1; JOINED.

DR EMBL; AC004257; AAC04897.1; --

DR EMBL; AC004663; AAC15789.1; ALT_INIT.

DR PIR; S78549; S78549.

DR HSSP; P00740; LEDM.

DR Genew; HGNC:7883; NOTCH3.

DR MIM; 600276; --

DR MIM; 125310; --

DR InterPro; IPR002110; ANK.

DR InterPro; IPR000152; Asx_hydroxyl_S.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001438; EGF_II.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR002049; Laminin_EGF.

DR InterPro; IPR008297; Notch.

DR InterPro; IPR000800; Notch_dom.

DR Pfam; PF00023; ank; 6.

DR Pfam; PF00008; EGF; 34.

DR PIRSF; PIRSF002279; Notch; 1.

DR PRINTS; PR00010; EGFBLD.

DR PRINTS; PR00011; EGF_LAMININ.

DR PRINTS; PR01452; NOTCH.

DR SMART; SM00248; ANK; 6.

DR SMART; SM00175; EGF_CA; 19.

DR SMART; SM00004; NL; 3.

DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.

DR PROSITE; PS50088; ANK_REPEAT; 4.

DR PROSITE; PS00010; ASX_HYDROXYL; 18.

DR PROSITE; PS00022; EGF_1; 33.

DR PROSITE; PS01186; EGF_2; 25.

DR PROSITE; PS50026; EGF_3; 34.

DR PROSITE; PS01187; EGF_CA; 16.

KW Receptor; Transcription regulation; Activator; Differentiation; Developmental protein; Repeat; ANK repeat; EGF-like domain; Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism; Disease mutation.

FT SIGNAL 1 39

FT CHAIN 40 2321

FT CHAIN 1629 2321

FT CHAIN 1662 2321

FT DOMAIN 40 1643

FT POTENTIAL.

FT NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 3.

FT NOTCH EXTRACELLULAR TRUNCATION (BY SIMILARITY).

FT NOTCH INTRACELLULAR DOMAIN (BY SIMILARITY).

FT EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 1644 1664 POTENTIAL.
FT DOMAIN 1665 2321 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 40 77 EGF-LIKE 1.
FT DOMAIN 78 118 EGF-LIKE 2.
FT DOMAIN 119 156 EGF-LIKE 3.
FT DOMAIN 158 195 EGF-LIKE 4.
FT DOMAIN 197 234 EGF-LIKE 5.
FT DOMAIN 236 272 EGF-LIKE 6.
FT DOMAIN 274 312 EGF-LIKE 7.
FT DOMAIN 314 350 EGF-LIKE 8.
FT DOMAIN 351 389 EGF-LIKE 9.
FT DOMAIN 391 429 EGF-LIKE 10.
FT DOMAIN 431 467 EGF-LIKE 11.
FT DOMAIN 469 505 EGF-LIKE 12.
FT DOMAIN 507 543 EGF-LIKE 13.
FT DOMAIN 545 580 EGF-LIKE 14.
FT DOMAIN 582 618 EGF-LIKE 15.
FT DOMAIN 620 655 EGF-LIKE 16.
FT DOMAIN 657 693 EGF-LIKE 17.
FT DOMAIN 695 730 EGF-LIKE 18.
FT DOMAIN 734 770 EGF-LIKE 19.
FT DOMAIN 771 808 EGF-LIKE 20.
FT DOMAIN 810 847 EGF-LIKE 21.
FT DOMAIN 849 885 EGF-LIKE 22.
FT DOMAIN 887 922 EGF-LIKE 23.

Alignment Scores:
Pred. No.: 0.0403 Length: 2321
Score: 98.50 Matches: 39
Percent Similarity: 30.56% Conservative: 5
Best Local Similarity: 27.08% Mismatches: 45
Query Match: 11.09% Indels: 55
DB: 1 Gaps: 5

US-09-773-476-294 (1-489) x NTF3_HUMAN (1-2321)
QY 52 TTTACAGGCTTATTACGTATTATCATGACCTTCAGGCAATCTCTCAAGGATGATT 111
Db 461 PheThrGlyThrTyrcys-----466
QY 112 GGCACACCTCCGCGTGGTGTACTCAGCTGCAGACTCTGTACTACACCAAGATGTTCC 171
Db 467 -----GluValAspIleAspGluCys-GlnSerSerPr 477
QY 172 CTGTCTCGAGGTAGTAATGCCTGGACAAATCTTCTTCAAG-----217
Db 477 OCysValAsnGlyGlyValCysLysAspArgValAsnGlyPheSerCysThrCysProSe 497
QY 218 -----GACAAGCAGATTTCAGAGGCAAGGACCTTTGCAATAGCACTGGAAGGCC 270
Db 497 rGlyPheSerGlySerThrCysGlnLeuAspValAspGluCysAlaSerThr-----514
QY 271 AGAATGTCTCTGAGAACGATCTTGTGCATCTGACGCTCTGCTTTTCAGTGGCT 330
Db 515 -----ProCys---ArgAsnGlyAlaLysCysValAspGlnProAspGlyTyrgluCysAr 532
QY 331 TTGTGCTGATGTTTCCATGATACAAAGTGTATGAGGCAG-----370
Db 532 gCysAlaGluGlyPheGluGlyThrLeuCysAspArgAsnValAspAspCysSerProAs 552
QY 371 -----GGCTCATTTTCACTGCTTATGTTCTT 396
Db 552 pProCysHisHisGlyArgCysValAspGlyIleAlaSerPheSer-CysAlaCysAlap 572
QY 397 TGGGATTC 404
Db 572 roGlyTyR 574
```

Search completed: June 25, 2004, 09:14:38
Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: June 25, 2004, 09:10:13 ; Search time 44 Seconds
(without alignments)
7013.109 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 888

Sequence: 1 gactgagctgattcttcag.....tnatgaccacacaagactt 489

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2034082

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-O/cgn2.1/USPTC_spool_p/US09773476/runat_25062004.090846.5828/app_query.fasta_1.647
-DB=SPREMBL_25 -QFWI=fastan -SUFFIX=n2p.rspt -MINMATCH=0.1 -LOOPEXT=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09773476 @CGN 1.1.86 @runat_25062004.090846.5828 -NCPU=6 -ICPU=3
-NC MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: sp archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	807	90.9	162 11 Q810Q3	Q810q3 mus musculu

RESULT 1					
Q810Q3	Q810Q3	PRELIMINARY;	PRT;	162 AA.	
ID	Q810Q3;				
AC	Q810Q3;				
DT	01-JUN-2003 (TrEMBLrel. 24, Created)				
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Similar to apoptosis related protein APR-3.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RA	Strausberg R.;				
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC049637; AAH49637.1; -.				
DR	InterPro; IPR006209; EGF-like.				
DR	PROSITE; PS00022; EGF_1; 1.				
DR	PROSITE; PS01186; EGF_2; 1.				
SQ	SEQUENCE 162 AA; 17519 MW; AD9498698BA1B71D CRC64;				

Alignment Scores: 4.5e-86 Length: 162
Pred. No.: 1

Q9dd14 mus musculu
Q9y2r7 homo sapien
Q96f16 homo sapien
Q96tr2 homo sapien
Q9y5l7 homo sapien
Q8klc3 mus musculu
Q962w9 podocoryne
Q7t52 mus musculu
Q7td51 mus musculu
Q8k428 mus musculu
Q7t50 mus musculu
Q810h2 mus musculu
Q800e4 brachydanio
Q46370 bos taurus
Q9u0e2 tribolium c
Q75412 homo sapien
Q00508 homo sapien
Q19350 caenorhabdi
Q61230 lytechinus
Q8n369 homo sapien
Q8ter0 homo sapien
Q9ded0 gallus gall
Q8k490 mus musculu
Q8k491 mus musculu
Q25253 lucilia cup
Q8i499 cupiennius
Q35806 rattus norv
Q9da37 brachydanio
Q96dw5 homo sapien
Q969r6 homo sapien
Q20852 caenorhabdi
Q8t4n9 strongyloce
Q9p3a5 brachiosto
Q61240 halocynthia
Q88840 mus musculu
Q9i594 xenopus lae
Q8t4p0 lytechinus
Q80ya8 mus musculu
Q80y0 mus musculu
Q16004 lytechinus
Q9wh9 rattus norv
Q51126 cryptospori
Q7y560 cryptospori
Q86pp7 cryptospori

Score: 807.00 Matches: 153
Percent Similarity: 98.71% Conservative: 0
Best Local Similarity: 98.71% Mismatches: 2
Query Match: 90.88% Indels: 1
DB: 11 Gaps: 0

US-09-773-476-294 (1-489) x Q81003 (1-162)

QY 6 AGGCTAGATCTTCAGACTGTCCTCTGAG-GATCCTGGTCCAAACTTTTACAGGCTTAT 64
Db 7 ArgLeuAspLeuGlnAsnCysSerLeuLeuAspProGlyProAsnPheLeuGlnAlaTyr 26
QY 65 ACTGCTATTATCATAGACCTTCAGGCAATCTCTCAAGATGATTTGGCCACACCTTC 124
Db 27 ThrAlaIleIleAspLeuGlnAlaAsnProLeuLeuAspAspLeuAlaAsnThrPhe 46
QY 125 CGTGGGTTTACTCAGCTGCAGACTCTCATACTACCAAGATGTCCTGTCTCTGAGGT 184
Db 47 ArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnAspValProCysProGlyGly 66
QY 185 AGTAATCCCTGGGCAATGTTACTCTCTTCAAGCAAGCAGATTTGCCAAGGCAAGG 244
Db 67 SerAsnAlaTrpAspAsnValThrSerPheLeuAspGlnIleCysGlnGlyGlnArg 86
QY 245 GACCTTTGCAATAGCACTGGAAGCCAGAAATGTCTGAGAACGATCTTCTGCTCATCT 304
Db 87 AspLeuCysAsnSerThrGlySerProGluMetCysProGluAsnGlySerCysAlaSer 106
QY 305 GACGGTCTCTCTTTGCAAGTGGTGTGCTGATGTTTCCATGATCAAGTCTATG 364
Db 107 AspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrCysMet 126
QY 365 AGGAGAGGCTCATTTTCACTGCTTATGTTCTTGGGATCTTGGATCCACCGCTAGCC 424
Db 127 ArgGlnGlySerPheSerLeuLeuMetPhePheGlyLeuLeuGlySerThrThrLeuAla 146
QY 425 ATCTNCATTTCTACTTTGGGAAACCCAGCGCCGCGAAAGCCAGGCT 469
Db 147 IleSerIleLeuLeuTrpGlyThrGlnArgArgGlyAlaLysAla 161

RESULT 2
Q9DD14 PRELIMINARY; PRT; 223 AA.
AC Q9DD14;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE G610007C2IRik protein.
GN APR3 OR 0610007C2IRIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
[1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirf L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK002276; BAB21981.1; -.
DR MGD; MGI:1918918; Apr3
DR InterPro; IPR006209; EGF-like.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
KW EGF-like domain.
SQ SEQUENCE 223 AA; 23867 MW; A85E3A03C7DD2C16 CRC64;

Alignment Scores:
Pred. No.: 9,47e-85 Length: 223
Score: 796.00 Matches: 152
Percent Similarity: 98.08% Conservative: 1
Best Local Similarity: 97.44% Mismatches: 3
Query Match: 89.64% Indels: 1
DB: 11 Gaps: 0

US-09-773-476-294 (1-489) x Q9DD14 (1-223)

QY 3 CTGAGGCTAGATCTTCAGAACTGTTCCCTGAG-GATCCTGGTCCAAACTTTTACAGGCT 61
Db 67 LeuGlyLeuAsnLeuGlnAsnCysSerLeuLeuAspProGlyProAsnPheLeuGlnAla 86
QY 62 TATCTGCTATTATCATAGACCTTCAGGCAATCTCTCAAGATGATTTGGCCAAACCC 121
Db 87 TyrThrAlaIleIleAspLeuGlnAlaAsnProLeuLeuAspAspLeuAlaAsnThr 106
QY 122 TTCGCTGGTGTACTCTGAGCTGCAGCTCTGATCTACCAAGATGTTCCCTGTCTCTGGA 181
Db 107 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnAspValProCysProGly 126
QY 182 GGTAGTATGCTGGGCAATGTTACTTCTTCAAGGACCAAGCAGATTTCCCAAGGCCAA 241
Db 127 GlySerAsnAlaTrpAspAsnValThrSerPheLeuAspGlnIleCysGlnGlyGln 146
QY 242 AGGACCTTTCCAACTAGCACTGGAAGCCAGAAATGTCTGAGAACGATCTTGTGCA 301
Db 147 ArgAspLeuCysAsnSerThrGlySerProGluMetCysProGluAsnGlySerCysAla 166
QY 302 TCTGACGGTCTCTGCTCTTCTTTCAGTGGGTTTGTCTGATGTTTCCATGGATCAAGTGT 361
Db 167 SerAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 186
QY 362 ATGAGGAGGCTCATTTTCACTGCTTATGTTCTTGGGATCTGGGATCCACACGCTA 421
Db 187 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyLeuLeuGlySerThrLeu 206
QY 422 GCCATCTTCATCTTCTACTTTGGGAAACCCAGCGCCGCGAAAGCCAGGCT 469
Db 207 AlaIleSerIleLeuLeuTrpGlyThrGlnArgArgGlyAlaLysAla 222

RESULT 3
Q9Y2R7 PRELIMINARY; PRT; 171 AA.
AC Q9Y2R7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-2003 (TrEMBLrel. 23, Last annotation update)
DE HSPC013 (Apoptosis related protein APR-3).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
[1]
NCBI_TaxID=9606;
SEQUENCE FROM N.A.
RP MEDLINE=20499367; PubMed=11042152;
RX Zhang Q.H., Ye M., Wu X.Y., Ren S.X., Zhao M., Zhao C.J., Fu G.,
RA Shen Y., Fan H.Y., Lu G., Zhong M., Xu X.R., Han Z.G., Zhang J.W.,

RA Tao J., Huang Q.H., Zhou J., Hu G.X., Gu J., Chen S.J., Chen Z.;
 RT "Cloning and functional analysis of cDNAs with open reading frames for
 ET 300 previously undefined genes expressed in CD34+ hematopoietic
 stem/progenitor cells";
 RL Genome Res. 10:1546-1560(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF077037; AAD27770.1; -;
 DR EMBL; BC035850; AAH35850.1; -;
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 KW EGF-like domain.
 SQ SEQUENCE 171 AA; 18597 MW; 91A42CD2B2CB0883 CRC64;
 Alignment Scores:
 Pred. No.: 2,876-72 Length: 171
 Score: 690.00 Matches: 128
 Percent Similarity: 89.68% Conservative: 11
 Best Local Similarity: 82.58% Mismatches: 16
 Query Match: 77.70% Indels: 1
 DB: 4 Gaps: 0
 US-09-773-476-294 (1-489) x Q9Y2R7 (1-171)
 QY 3 CTGAGGCTAGACTCTCAGACAGTTCCT-GAGGATCCTGTCGAACTTTTACAGGCT 61
 Db 15 LeuGlyLeuAspLeuGlnAsnProGlyProAsnPheHisGlnAla 34
 QY 62 TATACCTGCTATTATCATAGACCTTCAGGCAATCCTCTCAAGGATGATTGGCCAAACACC 121
 Db 35 HisThrThrValIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 54
 QY 122 TTCCTGGGTTTACTCAGCTGAGACTCTGATCTACTACACAGATGTTCCCTGCTCTGGA 181
 Db 55 PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnProGly 74
 QY 182 GGTAGTATGCTGGGCAATGTTACTTCTTCAAGGACACAGACATTTGCCAGGGCAA 241
 Db 75 GlyIleAsnAlaTrpAsnThrIleThrSerTyrlleAspAsnGlnIleCysGlnGlyGln 94
 QY 242 AGGACCTTTGCAATAGCACTGGAAGCCGAGAAATGTGTCCTGAGAACGGATCTTGTCGA 301
 Db 95 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 114
 QY 302 TCTGACGGTCCGTCTTTTTCAGTGGCTTGTGCTGATGTTTCCATGGATACAGTGT 361
 Db 115 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrlLysCys 134
 QY 362 ATGAGGAGGGCTCATTTTCTACCTGCTTATGTTCTTTGGGATTCGGATCCACACGCTA 421
 Db 135 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 154
 QY 422 GCATCTNCATTTCTACTTTGGGAAACCCAGCCCGGAAAGCCCAAG 466
 Db 155 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 169
 RESULT 4
 Q96FF6 PRELIMINARY; PRT; 229 AA.
 ID Q96FF6
 AC Q96FF6
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC011006; AAH11006.1; -;
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 KW Hypothetical protein; EGF-like domain.
 SQ SEQUENCE 229 AA; 24688 MW; F2C63F934A47ED33 CRC64;
 Alignment Scores:
 Pred. No.: 3,036-72 Length: 229
 Score: 690.00 Matches: 128
 Percent Similarity: 89.68% Conservative: 11
 Best Local Similarity: 82.58% Mismatches: 16
 Query Match: 77.70% Indels: 1
 DB: 4 Gaps: 0
 US-09-773-476-294 (1-489) x Q96FF6 (1-229)
 QY 3 CTGAGGCTAGACTCTCAGACAGTTCCT-GAGGATCCTGTCGAACTTTTACAGGCT 61
 Db 73 LeuGlyLeuAspLeuGlnAsnProGlyProAsnPheHisGlnAla 92
 QY 62 TATACCTGCTATTATCATAGACCTTCAGGCAATCCTCTCAAGGATGATTGGCCAAACACC 121
 Db 93 HisThrThrValIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
 QY 122 TTCCTGGGTTTACTCAGCTGAGACTCTGATCTACTACCAAGATGTTCCCTGCTCTGGA 181
 Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnProGly 132
 QY 182 GGTAGTATGCTGGGCAATGTTACTTCTTCAAGGACACAGACATTTGCCAGGGCAA 241
 Db 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrlleAspAsnGlnIleCysGlnGlyGln 152
 QY 242 AGGACCTTTGCAATAGCACTGGAAGCCGAGAAATGTGTCCTGAGAACGGATCTTGTCGA 301
 Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
 QY 302 TCTGACGGTCCGTCTTTTTCAGTGGCTTGTGCTGATGTTTCCATGGATACAGTGT 361
 Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrlLysCys 192
 QY 362 ATGAGGAGGGCTCATTTTCTACCTGCTTATGTTCTTTGGGATTCGGATCCACACGCTA 421
 Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
 QY 422 GCATCTNCATTTCTACTTTGGGAAACCCAGCCCGGAAAGCCCAAG 466
 Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227
 RESULT 5
 Q96RT2 PRELIMINARY; PRT; 171 AA.
 ID Q96RT2
 AC Q96RT2
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE P18 protein.
 GN P18.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang Y.C., Chen S.Y., Chang M.S.;

RT "Cloning and characterization of p18."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF275744; AA69412.1; -
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 KW EGF-like domain.
 SQ SEQUENCE 171 AA; 18567 MW; 81A52CD2B2CE0883 CRC64;

Alignment Scores:
 Pred. No.: 1,12e-71 Length: 171
 Score: 685.00 Matches: 127
 Percent Similarity: 89.03% Conservatives: 11
 Best Local Similarity: 81.94% Mismatches: 17
 Query Match: 77.14% Indels: 1
 DB: 4 Gaps: 0

US-09-773-476-294 (1-489) x Q96RT2 (1-171)

```

QY 3 CTGAGGCTAGATCTTCAGAACTGTCCTCCT-GAGGATCCTGGTCCAAACTTTTACAGGCT 61
DB 15 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 34
QY 62 TATACCTGCTATTATCATAGACCTTCAGGCAAACTCCTCTCAAGGATGATTGGCCAAACACC 121
DB 35 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 54
QY 122 TTCGGTGGGTTTACTCAGCTGCGAGCTGATACCTACCAAGATGTCCTGCTCCTGGA 181
DB 55 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 74
QY 182 GGTAGTAAATCCCTGGGCAATGTTACTTCTTCAAGGACAAAGCAGATTTGCCAAGGGCAA 241
DB 75 GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln 94
QY 242 AGGACCTTTTCAATAGCATGAGCCAGCAAAATGTGCTGAGAACGCGATCTTGTGCA 301
DB 95 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 114
QY 302 TCTGACGCTCCTGCTCTTTTCAGTGGCTGTTGCTGATGCTTCCATGGATCAACAGTGT 361
DB 115 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 134
QY 362 ATGAGGAGGCGCTATTTTCACGCTTATGTTCTTTGGGATTTGGGATCCACGCTA 421
DB 135 MetArgGlySerPheSerLeuLeuMetPheGlyLeuLeuGlyAlaThrThrLeu 154
QY 422 GCCATCTNCATTTCTACTTTGGGGAACCCAGCGCGGAAAGCCCAAG 466
DB 155 SerValSerIleLeuLeuTrpAlaAlaGlnArgGlyAlaLys 169

```

RESULT 6

Q9Y5L7 PRELIMINARY; PRT; 208 AA.
 AC Q9Y5L7;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Apoptosis related protein APR-3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhu F., Yan W., Chai Y.B., Shao C., Peng W.D., Yang A.G., Wang C.J.,
 RA Zhao Z.L.;
 RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF144055; AAD31317.2; -
 DR EMBL; AF144055; AAD31317.2; -
 SQ SEQUENCE 208 AA; 22687 MW; CD4C5723C62CAF6F CRC64;

Alignment Scores:

Pred. No.: 6,13e-65 Length: 208
 Score: 628.00 Matches: 122
 Percent Similarity: 82.82% Conservatives: 13
 Best Local Similarity: 74.85% Mismatches: 28
 Query Match: 70.72% Indels: 2
 DB: 4 Gaps: 0

US-09-773-476-294 (1-489) x Q9Y5L7 (1-208)

```

QY 3 CTGAGGCTAGATCTTCAGAACTGTCCTCCT-GAGGATCCTGGTCCAAACTTTTACAGGCT 61
DB 39 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 58
QY 62 TATACCTGCTATTATCATAGACCTTCAGGCAAACTCCTCTCAAGGATGATTGGCCAAACACC 121
DB 59 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 78
QY 122 TTCGGTGGGTTTACTCAGCTGCGAGCTGATACCTACCAAGATGTCCTGCTCCTGGA 181
DB 79 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 98
QY 182 GSTAGTAAATCCCTGGGCAATGTTACTTCTTCAAGGACAAAGCAGATTTGCCAAGGGCAA 241
DB 99 GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln 118
QY 242 AGGACCTTTTCAATAGCATGAGCCAGCAAAATGTGCTGAGAACGCGATCTTGTGCA 301
DB 119 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 138
QY 302 TCTGACGCTCCTGCTCTTTTCAGTGGCTGTTGCTGATGCTTCCATGGATCAACAGTGT 360
DB 139 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyIleGlnVal 158
QY 361 TATCAGGAGGCGCTATTTTCACGCTTATGTTCTTTGGGATTTGGGATCCACGCT 420
DB 159 TyrAlaProGlyLeuValLeuThrAlaTyrValLeuArgAspSerGlySerHisHisSer 178
QY 421 AGCATCTNCATTTCTACTTTGGGGAACCCAGCGCGGAAAGCCCAAGCTTATGAGCCAC 480
DB 179 IleArgLeuHisSerAlaLeuGlyGlyProAlaProLysSerGlnAspPheMetAsnTyr 198
QY 481 ACAAGACTT 489
DB 199 IleglyLeu 201

```

RESULT 7

Q8K1E3 PRELIMINARY; PRT; 382 AA.
 ID Q8K1E3
 AC Q8K1E3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to hypothetical protein MGC2487.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RA TISSUS=Salivary gland;
 RC Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC019431; AAH19431.1; -
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR InterPro; IPR000152; Asx_hydroxyl_S.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001881; EGF-Ca.
 DR InterPro; IPR001438; EGF II.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR002049; Laminin_EGF.

DR Pfam: PF00008; EGF_5.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00011; EGFBLAMIN.
DR SMART; SM00181; EGF_6.
DR SMART; SM00179; EGF_CA; 5.
DR PROSITE; PS00010; ASX HYDROXYL; 2.
DR PROSITE; PS00022; EGF_1; 6.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS01187; EGF_CA; 2.
KW Hypothetical protein; EGF-like domain.
SQ SEQUENCE 382 AA; 40404 MW; F2C82AD649CA0B3C CRC64;

Alignment Scores:
Pred. No.: 0.00114 Length: 382
Score: 109.00 Matches: 29
Percent Similarity: 37.65% Conservative: 3
Best Local Similarity: 34.32% Mismatches: 28
Query Match: 12.27% Indels: 25
DB: 11 Gaps: 4

US-09-773-476-294 (1-489) x Q8K1E3 (1-382)

QY 118 CACCTTCGCTGGTATTACTAGCTGCAGACTCTGATACCAAGATGTTCCCTGTC 177
Db 72 HisGlnProTTP-----GlnCysile-CysHI 80
QY 178 TGGAGTAGTAATGCTCGGACAAATGTTACTTCTTCAAGACAAAGCAGATTTGCCAAGG 237
Db 80 sSerGly-----TTPAlaGlyLysPheCysAspLysaspGluHisileCysThrSe 97
QY 238 GCAAGGACCTTTCATATAGCAGCTGGAAGCCGAGAAATGTGCTGAGAACGATCTTG 297
Db 97 rGln-----SerPro-----CysGlnAsnGlyGlyGlnC 107
QY 298 TGCATCTCAGCTGCTGCTTTTTCAGTGGTGTGCTGATGTTTCCATGATACAA 357
Db 107 sValTyraspGlyGlyGlyGlyGlyHisCysValCysLeuProGlyPheHisGlyArgGI 127
QY 358 GTGATAGGCAG 370
Db 127 yCysGluArgLys 131

RESULT 8
Q962W9 PRELIMINARY; PRT; 713 AA.
ID Q962W9
AC Q962W9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE EGF-like protein (Fragment).
OS Podocoryne carnea.
OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidea; Anthomedusae;
OC Hydractiniidae; Podocoryne.
OX NCBI_TaxID=6096;
RN [1]
RP SEQUENCE FROM N.A.
RA Bauer P.; Plickert G.;
RT "cDNA Cloning of a protein with EGF repeats (C-X4-C-X5-C-X8-C-X-C-X8-C-X6) from the hydroid Podocoryne carnea."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397902; AAK92130.1;
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000152; ASX_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002049; Laminin_EGF.
DR Pfam; PF00008; EGF_18.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00011; EGFBLAMIN.
DR SMART; SM00179; EGF_CA; 16.

DR PROSITE; PS00010; ASX HYDROXYL; 17.
DR PROSITE; PS00022; EGF_1; 18.
DR PROSITE; PS01186; EGF_2; 18.
DR PROSITE; PS01187; EGF_CA; 16.
KW EGF-like domain.
FT NON TER 1
SQ SEQUENCE 713 AA; 76908 MW; 980E392B533E42D0 CRC64;

Alignment Scores:
Pred. No.: 0.00147 Length: 713
Score: 108.50 Matches: 36
Percent Similarity: 41.03% Conservative: 12
Best Local Similarity: 30.77% Mismatches: 42
Query Match: 12.22% Indels: 27
DB: 5 Gaps: 7

US-09-773-476-294 (1-489) x Q962W9 (1-713)

QY 74 ATCATGACCTTCAGGCAAAATCTCTCAAGAT-----GATTTGGCCAAC 118
Db 81 IleAspGluCysAsnProAsnProCysLysAsnAsnAlaValCysSerAspIleValAsn 100
QY 119 ACCTTCGGT-----GGGTTTACTCAGCTGCAGACTCTGATACCAACAA 163
Db 101 GlyPheLysCysSerCysLeuProGlyPheThrGly---GluThrCysGluIleGluIle 119
QY 164 GAT-----GTTCCCTGCTCGAGGTAGTATGCTCGGACAAATGTTACTTCT 211
Db 120 AspGluCysSerSerSerProCysLeuAsnAlaAlaAsnCysThrAspLysValAsnAsp 139
QY 212 TTCAGGACAG-----CAGATTTGCCAAGGCAAGGACCTT 250
Db 140 PheGluCysLysCysLysProGlyTyThrGlyLysileCysGluThrAspIleAspGlu 159
QY 251 TGCAATAGCACTGGAAGCCGAGAAATGTGCTCGAGACGGATCTTGTGCATCTGACGGT 310
Db 160 CysAsn-----ProAsnProCysGlnAsnAsnAlaThrCys---SerAspLeu 174
QY 311 CTGGTCTTTTTCAGTGGTGTGCTGATGTTTCCATGATACAAAGTGT 361
Db 175 ValAsnGlyPheLysCysThrCysLeuAlaGlyPheThrGlyGluThrCys 191

RESULT 9
Q7TQ52 PRELIMINARY; PRT; 2516 AA.
ID Q7TQ52
AC Q7TQ52
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transmembrane receptor Notch1 B.
GN NOTCH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C.B-17; TISSUE=Thymus;
RA Tsuji H.; Iehai-Ohba H.; Ukai H.; Katsube T.; Ogii T.;
RT "Radiation-induced deletions in the 5' end region of Notch1 lead to the formation of truncated proteins and are involved in the development of mouse thymic lymphomas."
RL Carcinogenesis 24:1-12(2003).
DR EMBL; AB100603; BAC77038.1;
DR Receptor; Transmembrane.
KW Receptor; Transmembrane.
SQ SEQUENCE 2516 AA; 269177 MW; 17FD72740EBD6E35 CRC64;

Alignment Scores:
Pred. No.: 0.00479 Length: 2516
Score: 105.00 Matches: 41
Percent Similarity: 35.80% Conservative: 17
Best Local Similarity: 25.31% Mismatches: 53
Query Match: 11.82% Indels: 51

DR MGD; MGI:97363; Notch1.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0030154; P:cell differentiation; IMP.
DR GO; GO:0007386; P:compartment specification; IMP.
DR GO; GO:0045944; P:positive regulation of transcription from P. . . ; IDA.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx hydroxyl_s.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF-II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR008297; Notch.
DR InterPro; IPR000800; Notch_dom.
DR Pfam; PF00023; ank; 6.
DR Pfam; PF00008; EGF; 36.
DR Pfam; PF00066; notch; 3.
DR PRINTS; PR00010; EGFLEOOD.
DR PRINTS; PR00011; EGFLEAMIN.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 6.
DR SMART; SM00181; EGF; 37.
DR SMART; SM00179; EGF_CA; 35.
DR SMART; SM00004; NL; 3.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF 1; 35.
DR PROSITE; PS01186; EGF 2; 27.
DR PROSITE; PS01187; EGF_CA; 21.
DR PIRSF; PIRSF002279; Notch; 1.
KW ANK repeat; EGF-like domain; Repeat.
SQ SEQUENCE 2531 AA; 270819 MW; 7DB7E0DEF799D999 CRC64;

Alignment Scores:
Pred. No.: 0.0048 Length: 2531
Score: 105.00 Matches: 41
Percent Similarity: 35.80% Conservative: 17
Best Local Similarity: 25.31% Mismatches: 53
Query Match: 11.82% Indels: 51
DB: 11 Gaps: 8

US-09-773-476-294 (1-489) x Q8K428 (1-2531)

QY 53 TTACAGGCTTATCTGCT-----ATTATCATAGACCTTCAG-----GCAAACTCT 97
DB 441 LeuGlnGlyTyrThrGlyProArgCysGluIleAspValAsnGluCysIleSerAsnPro 460
QY 98 CTCAGAGGATGTTGGCCCAACACCTTCGCGTGGTTTACTACGCTGCAGCTCTGATACTA 157
DB 461 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysIleCysMet 479
QY 158 CCA-----CAAGATGTTCCCTGT 175
DB 480 ProGlyTyrGluGlyValTyrCysGluIleAsnThrAspGluCysAlaSerSerProCys 499
QY 176 CTGGAGGTAGTAATGCTGGGACAATGTTACTTCTTCAAG----- 217
DB 500 LeuHisAsnGlyHisCysMetAspLysIleAsnGluPheGlnCysGlnCysProLysGly 519
QY 218 ---GACAAGCAGATTGTCAGAGGCAAGGACCTTTCGATAGCAGCTGGAAGCCAGAA 274
DB 520 PheAsnGlyHisLeuCysGlnTyrAspValAspGluCysAlaSerThr----- 535
QY 275 ATGTGCTCCTGAGAACGATCTTGTGCATCTGACGCTCGCTGCTTTTGCAGTGGCTTGT 334
DB 536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys 554
QY 335 GCTGATGTTTCCATGATACAAAGTGT----- 361
DB 555 ThrGluGlyTyrThrGlyThrHisCysGluValAspIleAspGluCysAspProAspPro 574
QY 362 -----ATCAGCAGCGGCTCATTTTCACTGCTTATGTTCTTTGG 400

QY 362 -----ATGAGCAGCGGCTCATTTTCACTGCTTATGTTCTTTGG 400
DB 575 CysHisTyrGlySerCysLysAsp-GlyValAlaThrPheThrCysLeuCysGlnProGl 594
QY 401 ATTC 404
DB 594 YTYR 595
RESULT 12
Q7TQ50 PRELIMINARY; PRT; 2531 AA.
ID Q7TQ50
AC Q7TQ50;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Transmembrane receptor Notch1.
GN NOTCH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B-17; TISSUE=Thymus;
RA Tsuji H., Ishii-Ohba H., Ukai H., Katsube T., Ogizu T.;
RT "Radiation-induced deletions in the 5' end region of Notch1 lead to
RT the formation of truncated proteins and are involved in the
RT development of mouse thymic lymphomas.";
RL Carcinogenesis 24:1-12(2003).
DR EMBL; AB10603; BAC77040.1; -.
KW Receptor; Transmembrane.
SQ SEQUENCE 2531 AA; 270832 MW; 97C91F69BABF02BF CRC64;

Alignment Scores:
Pred. No.: 0.0048 Length: 2531
Score: 105.00 Matches: 41
Percent Similarity: 35.80% Conservative: 17
Best Local Similarity: 25.31% Mismatches: 53
Query Match: 11.82% Indels: 51
DB: 11 Gaps: 8

US-09-773-476-294 (1-489) x Q7TQ50 (1-2531)

QY 53 TTACAGGCTTATCTGCT-----ATTATCATAGACCTTCAG-----GCAAACTCT 97
DB 441 LeuGlnGlyTyrThrGlyProArgCysGluIleAspValAsnGluCysIleSerAsnPro 460
QY 98 CTCAGAGGATGTTGGCCCAACACCTTCGCGTGGTTTACTACGCTGCAGCTCTGATACTA 157
DB 461 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysIleCysMet 479
QY 158 CCA-----CAAGATGTTCCCTGT 175
DB 480 ProGlyTyrGluGlyValTyrCysGluIleAsnThrAspGluCysAlaSerSerProCys 499
QY 176 CTGGAGGTAGTAATGCTGGGACAATGTTACTTCTTCAAG----- 217
DB 500 LeuHisAsnGlyHisCysMetAspLysIleAsnGluPheGlnCysGlnCysProLysGly 519
QY 218 ---GACAAGCAGATTGTCAGAGGCAAGGACCTTTCGATAGCAGCTGGAAGCCAGAA 274
DB 520 PheAsnGlyHisLeuCysGlnTyrAspValAspGluCysAlaSerThr----- 535
QY 275 ATGTGCTCCTGAGAACGATCTTGTGCATCTGACGCTCGCTGCTTTTGCAGTGGCTTGT 334
DB 536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys 554
QY 335 GCTGATGTTTCCATGATACAAAGTGT----- 361
DB 555 ThrGluGlyTyrThrGlyThrHisCysGluValAspIleAspGluCysAspProAspPro 574
QY 362 -----ATCAGCAGCGGCTCATTTTCACTGCTTATGTTCTTTGG 400

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Db 575 CysHisTyrGlySerCysLysAsp-GlyValAlaThrPheThrCysLeuCysGlnProgl 594
QY 401 ATTC 404
Db 594 YTYR 595
RESULT 13
ID Q810H2 PRELIMINARY; PRT; 1065 AA.
AC Q810H2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Secreted protein SST3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Ueno H.;
RT "A stomal cell-derived membrane protein that supports hematopoietic
stem cells.";
RL Nat. Immunol. 0:0-0(2003).
DR EMBL; AY169783; AAC41836.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0007160; P:cell-matrix adhesion; IEA.
DR InterPro; IPRO00152; Asx hydroxyl_S.
DR InterPro; IPRO00742; EGF_2.
DR InterPro; IPRO01881; EGF_Ca.
DR InterPro; IPRO01438; EGF_II.
DR InterPro; IPRO06209; EGF_like.
DR InterPro; IPRO03961; FN_III.
DR InterPro; IPRO06210; IEGF.
DR InterPro; IPRO02049; Laminin_EGF.
DR InterPro; IPRO03886; Nidogen_ext.
DR InterPro; IPRO00436; Sushi_SCR_CCP.
DR Pfam; PF00008; EGF; 13.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00084; sushi; 1.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00011; EGF_LAMININ.
DR SMART; SMC0032; CCP; 1.
DR SMART; SMC0181; EGF; 14.
DR SMART; SMC0179; EGF_CA; 13.
DR SMART; SMC0060; FN3; 1.
DR SMART; SMC0539; NIDO; 1.
DR PROSITE; PS00010; ASX HYDROXYL; 6.
DR PROSITE; PS00022; EGF_1; 14.
DR PROSITE; PS01186; EGF_2; 13.
DR PROSITE; PS01187; EGF_CA; 3.
SQ SEQUENCE 1065 AA; 114283 MW; 899E199051139D80 CRC64;

Alignment Scores:
Pred. No.: 0.00468 Length: 1065
Score: 104.50 Matches: 37
Percent Similarity: 29.86% Conservative: 6
Best Local Similarity: 25.69% Mismatches: 33
Query Match: 11.77% Indels: 68
Deby: 11 Gaps: 7

US-09-773-476-294 (1-489) x Q810H2 (1-1065)
QY 161 CAAGATGTCCTGCTCGAGTAGTAATGCTGGGCAATGTTACTTCTTCAGGAC 220
Db 796 GlnAlaGlnProCysArgAsnGlySerCysArgAspLeuProArgAlaPhe----- 813
QY 221 AAGCAGATTGGCAA-----GGGCAAAAGGAC 247
Db 814 -----IleCysGlnCysProGluGlyPheValGlyIleHisCysGluThrGluValAsp 831
QY 248 CTTTGAATAGCACTGGAAGCCAGAAATGTCCTGTGAGACGGATCTTGTCATCTGAC 307

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Db 832 AlaCysAlaSer-----SerPro-----CysGlnHisGlyGlyArgCys---GluAsp 846
QY 308 GGTCTGCTGTTTTCAGTGGCTTGTGCTGATGGTTTCCATGATACAGTGT----- 361
Db 847 GlyGlyGlyAlaTyrLeuCysValCysProGluGlyPhePheGlyTyrAsnCysGluThr 866
QY 362 -----ATGAGGCAG 370
Db 867 MetSerAspProCysPheSerSerProCysGlySerArgGlyTyrCysLeuAlaSerAsn 886
QY 371 GGCTCATTTTCACGTGCTTATGTTCTTTGGGATTC----- 404
Db 887 GlySerHisSer-CysThrCysLysValGlyTyrThrGlyLysAspCysThrLysGluLe 906
QY 405 -----TG 406
Db 906 uLeuProProThrAlaLeuArgValGluArgValGluSerGlyValSerIleSerTr 926
QY 407 GGATCCACCA 416
Db 926 pSerProPro 929
RESULT 14
ID Q800E4 PRELIMINARY; PRT; 2468 AA.
AC Q800E4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Notch3.
GN NOTCH3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim C.-H., Chitnis A.;
RT "Zebrafish Notch3 and Neural Plate Formation.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152001; AAF73197.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0030154; P:cell differentiation; IEA.
DR InterPro; IPRO02110; ANK.
DR InterPro; IPRO00152; Asx hydroxyl_S.
DR InterPro; IPRO00742; EGF_2.
DR InterPro; IPRO01881; EGF_Ca.
DR InterPro; IPRO01438; EGF_II.
DR InterPro; IPRO06209; EGF_like.
DR InterPro; IPRO01092; HLH_basic.
DR InterPro; IPRO06210; IEGF.
DR InterPro; IPRO02049; Laminin_EGF.
DR InterPro; IPRO08297; Notch.
DR InterPro; IPRO08000; Notch_dom.
DR InterPro; IPRO01673; S_mold_repeat.
DR Pfam; PF00023; ank; 6.
DR Pfam; PF00008; EGF; 35.
DR Pfam; PF00066; notch; 3.
DR PRINTS; PR00010; EGFBL00D.
DR PRINTS; PR00011; EGF_LAMININ.
DR PROSITE; PS01452; NOTCH.
DR PROSITE; PS00686; S_mold_repeat; 1.
DR SMART; SMC0248; ANK; 6.
DR SMART; SMC0181; EGF; 35.
DR SMART; SMC0179; EGF_CA; 33.
DR SMART; SMC0004; NL; 3.
DR PROSITE; PS00088; ANK_REPEAT; 4.
DR PROSITE; PS00297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.

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DR PROSITE; PS00022; EGF_1; 34.
DR PROSITE; PS01186; EGF_2; 30.
DR PROSITE; PS01187; EGF_3A; 20.
DR PROSITE; PS00038; HLH_1; 1.
DR PIRSF; PIRSF002279; Notch; 1.
SQ SEQUENCE 2468 AA; 266643 MW; F147966714EP946B CRC64;

Alignment Scores:
Pred. No.: 0.00942 Length: 2468
Score: 102.50 Matches: 34
Percent Similarity: 39.85% Conservative: 19
Best Local Similarity: 25.56% Mismatches: 47
Query Match: 11.54% Indels: 33
DB: 13 Gaps: 9

US-09-773-476-294 (1-489) x Q800E4 (1-2468)

QY 44 CCAAACTTTTACAGCGCTTACTCTATTATCATAGAC---CTTCAGGCAAACTCTCTC 100
DB 435 ProGlyTyrGlnGlyLysTyrCysGluValAspIleAspGluCysGluSerAsnProCys 454
QY 101 AAGGAT-----GATTGGCCCAACACTTCCGT-----GGG 130
DB 455 ValAsnAspGlyLeCysArgAspMetValAsnGlyPheThrCysThrCysGlnProGly 474
QY 131 TTTACTAGCTCAGACTCTGATCTACTACACAGATGT-----CCC 172
DB 475 PheThrGlyThrMetCysGlnIle-----AspIleAspGluCysAlaSerThrPro 491
QY 173 TGCTCTGGAGGTAGTAATGCTGGGCAATGTTACTTCTTCAAG-----217
DB 492 CysGlnAsnGlyAlaLysCysIleAspArgProAsnGlyTyrGluCysArgCysAlaGlu 511
QY 218 -----GACAACGAGATTGCCAAGGCAAGGACCTTTTGCATAGCACTGGAGGCCCA 271
DB 512 GlyPheGluGlyArgLeuCysGluSerAsnIleAspAsnCys-----LysPro 527
QY 272 GAAATCTGTCCTGAGAACGATCTGTGCATCTGACGGTCCTGTCCTTTTGCAGTGCCTT 331
DB 528 AspProCys---HisHisGlyThrCysVal---AspGlyIleAlaSerTyrThrCysAsn 545
QY 332 TGCTGTGATGGTTTCATGATACCAAGTGTATGAGGCAG 370
DB 546 CysGluProGlyTyrThrGlyTyrArgCysGluAsnGln 558

RESULT 15
O46370 PRELIMINARY; FRT; 308 AA.
AC O46370;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Preadipocyte factor-1.
GN DLK.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fat;
RA Minoshima Y., Taniguchi Y., Sasaki Y.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Fahrenkrug S.C., Freking B.A., Smith T.P.S.;
RT "Genomic Organization and Chromosomal Position of the Bovine DLK
Gene."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB009278; BAA23733.1; -
DR EMBL; AF181466; AAF00926.1; -
DR EMBL; AF181463; AAF00926.1; JOINED.

Search completed: June 25, 2004, 09:16:14
Job time : 50 secs

Search completed: June 25, 2004, 09:16:14
Job time : 50 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 25, 2004, 09:10:48 ; Search time 20 Seconds
(without alignments)
2524.510 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 888

Sequence: 1 gactgagctgattcttcag.....tntatgagccacacaagactt 489

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778828

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents AA -QFMT=fastan -SUFFIX=n2p.ra -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NOEM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09773476@cgn2_1_27@runat_25062004_090847_5856 -NCPU=6 -ICPU=3
-NO MAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
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5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	336	37.8	165	4 US-09-621-976-5263
2	273	30.7	79	4 US-09-621-976-6689
3	272	30.6	52	4 US-10-138-158-21
4	106.5	12.0	1964	4 US-09-467-997-1
5	102	11.5	1139	1 US-08-537-210A-4
6	102	11.5	1139	3 US-09-113-825-4
7	102	11.5	2471	1 US-08-185-432-16
8	102	11.5	2471	1 US-08-083-590A-19
9	102	11.5	2471	3 US-08-532-384-19
10	102	11.5	2471	4 US-08-899-232-1
11	102	11.5	2703	1 US-08-185-432-19
12	102	11.5	2703	4 US-08-899-232-4

ALIGNMENTS

RESULT 1

US-09-621-976-5263
; Sequence 5263, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Melne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5263
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 30...1
US-09-621-976-5263

Alignment Scores:

Pred. No.:	1,35e-30	Length:	165
Score:	336.00	Matches:	73
Percent Similarity:	83.16%	Conservative:	6
Best Local Similarity:	76.84%	Mismatches:	14
Query Match:	37.84%	Indels:	3
DB:	4	Gaps:	0

US-09-773-476-294 (1-489) x US-09-621-976-5263 (1-165)

QY 3 CTGAGGCTAGATCTTCAGACCTGTTCCCT-GAGGATCCTGTCACAACTTTTACGCT 61

Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92

Sequence 17, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 12, Appl
Patent No. 517197
Sequence 2, Appl
Sequence 2, Appl
Sequence 5, Appl
Sequence 7, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 11, Appl
Sequence 2, Appl
Sequence 8, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 8, Appl
Sequence 18, Appl
Sequence 3, Appl
Sequence 52, Appl
Sequence 52, Appl
Sequence 7, Appl
Sequence 6, Appl
Sequence 16, Appl

QY 128 GGGTTTACTCAGCTGAGACTCTGTATACACCAAGAT----- 166
Db 264 GlyPheThrGlyLeuAspCysGluMetAsnProAspAspCysValArgHisGlnCysGln 283
QY 167 -----GTTCCCTGCTCCTGGAGGTAGT 187
Db 284 AsnGlyAlaThrCysLeuAspGlyLeuAspThrTyThrCysProCysProLysThrTrp 303
QY 188 AATGCTGGGACAATGTTACTTCTTCAAGGACAAGCAGATTGGCAAGGGCAAGGGAC 247
Db 304 LysGlyTrpAsp-----CysSerGluAspIleAsp 313
QY 248 CTTTCAATAGACACTGAGACCCAGAAATGTTCTCTGAGAACGGATCTGTGCTCTGAC 307
Db 314 GluCysGluAlaArgGlyProProArg---CysA-gAsnGlyGlyThrCysGlnAsnThr 332
QY 308 GGTCTCTGCTGCTTTTGCAGTGCCTTTGCTGTATGTTTCCATGGATACAAAGTGTATG--- 364
Db 333 Ala---GlySerPheHisCysValCysValSerGlyTrpGlyGlyAlaGlyCysGluGlu 351
QY 365 -----AGGCAG 370
Db 352 AsnLeuAspAspCysAlaAlaAlaThrCysAlaProGlySerThrCysIleAspArgVal 371
QY 371 GGCTCATTTTCACTGCTTATGTTCTTTGGGA 401
Db 372 GlySerPheSer-CysLeuCysProProGly 381

RESULT 5
US-08-537-210A-4
; Sequence 4, Application US/08537210A
; Patent No. 5780300
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Fortini, Mark
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY
; TITLE OF INVENTION: DIFFERENTIATED CELLS USING THE NOTCH PATHWAY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/537,210A
; FILING DATE: 29-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,972
; REFERENCE/DOCKET NUMBER: 7326-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1139 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Dros N

; LOCATION: 1189...2327
; OTHER INFORMATION: Highly conserved ankyrin repeat
; OTHER INFORMATION: region of No. 5780300ch
US-08-537-210A-4
Alignment Scores:
Pred. No.: 0.00408 Length: 1139
Score: 102.00 Matches: 25
Percent Similarity: 42.25% Conservative: 5
Best Local Similarity: 35.21% Mismatches: 29
Query Match: 11.49% Indels: 12
DB: Gaps: 3
US-09-773-476-294 (1-489) x US-08-537-210A-4 (1-1139)
QY 170 CCTGTCTCTGAGGTAGTAATGCTGGGACAATGTTACTTCTTCAAGGACAAG----- 223
Db 41 ProCysGlnAsnGlyGlyThrCysHisAspArgValMetAsnPheSerCysSerCysPro 60
QY 224 -----CAGATTGCGAAGGCAAGGACCTTTGCAATAGCACTGGAAGC 268
Db 61 ProGlyThrMetGlyIleIleCysGluIleAsnLysAspAspCys-----Lys 76
QY 269 CCAGAAATGTCTCTGAGAACGGATCTTGTGCATCTGACGGTCTGTGCTCTTTTGCAGTGC 328
Db 77 ProGlyAlaCysHisAsnAsnGlySerCysIle---AspArgValGlyGlyPheGluCys 95
QY 329 GTTTGCTGCTGATGCTTTTCCATGGATACAAAGTGT 361
Db 96 ValCysGlnProGlyPheValGlyAlaArgCys 106
RESULT 6
US-09-113-825-4
; Sequence 4, Application US/09113825
; Patent No. 6149902
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Fortini, Mark
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: MANIPULATION OF NON-TERMINALLY
; TITLE OF INVENTION: DIFFERENTIATED CELLS USING THE NOTCH PATHWAY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/113,825
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 08/537,210
; FILING DATE: 29-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,972
; REFERENCE/DOCKET NUMBER: 7326-027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1139 amino acids
; TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Dros N 2327
LOCATION: 1189-2327
OTHER INFORMATION: Highly conserved ankyrin repeat
OTHER INFORMATION: region of No. 6149902ch
US-09-113-825-4

Alignment Scores:
Pred. No.: 0.00408 Length: 1139
Score: 102.00 Matches: 25
Percent Similarity: 42.25% Conservativity: 5
Best Local Similarity: 35.21% Mismatches: 29
Query Match: 11.49% Indels: 12
DB: 3 Gaps: 3

US-09-773-476-294 (1-489) x US-09-113-825-4 (1-1139)

QY 170 CCTGTCTGGAGTAGTAATGCTGGACAATGTTACTTCTTCAAGGACAG----- 223
Db 41 ProCysGlnAsnGlyGlyThrCysHisAspArgValMetAsnPheSerCysSerCysPro 60
QY 224 -----CAGATTGCGAAGGCGAAGGACCTTTGCAATAGCACTGGAAGC 268
Db 61 ProGlyThrMetGlyIleIleCysGluIleAsnLysAspAspCys-----Lys 76
QY 269 CCAGAAATGTCTCGAAGCGATCTTGTGCATCTGACGGTCTGTTTTCGAGTGC 328
Db 77 ProGlyAlaCysHisAsnAsnGlySerCysIle---AspArgValGlyGlyPheGluCys 95
QY 329 GTTGTGTGTGATGTTTCCATGGATACAAGT 361
Db 96 ValCysGlnProGlyPheValGlyAlaArgCys 106

RESULT 7

US-08-185-432-16
Sequence 16, Application US/08185432
Patent No. 5750652
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
APPLICANT: Busseau, Isabelle
APPLICANT: Diederich, Robert J.
APPLICANT: Xu, Tian
APPLICANT: Matsuno, Kenji
TITLE OF INVENTION: DELTA PROTEINS, NUCLEIC ACIDS, AND
TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/185,432
APPLICATION NUMBER: US/08/185,432
FILING DATE: 21-JAN-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7326-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:
LENGTH: 2471 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-185-432-16

Alignment Scores:
Pred. No.: 0.0054 Length: 2471
Score: 102.00 Matches: 42
Percent Similarity: 36.18% Conservativity: 13
Best Local Similarity: 27.63% Mismatches: 48
Query Match: 11.49% Indels: 49
DB: 1 Gaps: 8

US-09-773-476-294 (1-489) x US-08-185-432-16 (1-2471)

QY 74 ATCATAGACTTCAAGCAATCTCTCAAGGAT-----GATTGGCCCAAC 118
Db 912 IleAspAspCysLeuAlaAsnProCysGlnAsnGlyGlySerCysMetAspGlyValAsn 931
QY 119 ACCTTCCGT-----GGTTTACT-----CAGCTGCAGACTCTGATCTA 157
Db 932 ThrPheSerCysLeuCysLeuProGlyPheThrGlyAspLysCysGlnThr----- 948
QY 158 CCACAAGATGT-----CCCTGTCTCTGGAGGTAGTATGCTCTGGAC 199
Db 949 -----AspMetAsnGluCysLeuSerGluProCysLysAsnGlyGlyThrCysSerAsp 966
QY 200 AATGTTACTTCTTCAAGCAAGCAGATTTCACAAAGGCGAAGGACCTTTGCAATAGC 259
Db 967 TyrValAsnSerTyrThrCysLys-----CysGlnAlaGlyPheAspGlyValHisCys 984
QY 260 ACTGGAAGCCCAAGAAATGTCTCTGAG-----AACGGATCTGTGCACTCTGAC 307
Db 985 GluAsnAsnIleAsnGluCysThrGluSerSerCysPheAsnGlyGlyThrCysValAsp 1004
QY 308 GGTCTCTGTCTTTTGCAGTGGCTTTGTGCTGATGGTTTCCATGGATACAACTGATGAGG 367
Db 1005 GlyIleAsnSerPheSerCysLeuCysProValGlyPheThrGlySerPheCysLeuHis 1024
QY 368 CAG----- 370
Db 1025 GluIleAsnGluCysSerSerHisProCysLeuAsnGluGlyThrCysValAspGlyLeu 1044
QY 371 GGCTCATTTTCACTGCTTATGTTCTTTGGATTC 404
Db 1045 GlyThr-TyrArgCysSerCysProLeuGlyTyr 1055

RESULT 8

US-08-083-590A-19
Sequence 19, Application US/08083590A
Patent No. 5786158
GENERAL INFORMATION:

APPLICANT: Artavanis-Tsakonas, S. et al.
TITLE OF INVENTION: Therapeutic And Diagnostic Methods
TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
TITLE OF INVENTION: Nucleic Acids
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/083,590A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 8698864/9741
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-083-590A-19

Alignment Scores:
Pred. No.: 0.0054 Length: 2471
Score: 102.00 Matches: 42
Percent Similarity: 36.18% Conservative: 13
Best Local Similarity: 27.63% Mismatches: 48
Query Match: 11.49% Indels: 49
DB: 1 Gaps: 8

US-09-773-476-294 (1-489) x US-08-083-590A-19 (1-2471)
QY 74 ATCATAGACTTCAGCAAAATCTCTCAAGAT-----GATTGGCCCAAC 118
Db 912 IleAspAspCysLeuAlaAsnProCysGlnAsnGlySerCysMetAspGlyValAsn 931
QY 119 ACCTTCGGT-----GGGTTTACT-----CAGCTGCAGACTCTGATACTA 157
Db 932 ThrPheSerCysLeuCysLeuSerGluProGlyPheThrGlyAspLysCysGlnThr 948
QY 158 CCACAGATGTT-----CCCTGTCTGGAGGTAGTAAATGCTGGGAC 199
Db 949 -----AspMetAsnGluCysLeuSerGluProCysLysAsnGlyThrCysSerAsp 966
QY 200 AATGTTACTCTTTCAGGACAGCAGATTGCCAGGCAAGGACCTTTGCAATAGC 259
Db 967 TyrValAsnSerTyrThrCysLys-----CysGlnAlaGlyPheAspGlyValHisCys 984
QY 260 ACTGGAAGCCAGAAATGTCTCTGAG-----AACGGATCTTGTGCATCTGAC 307
Db 985 GluAsnAsnIleAsnGluCysThrGluSerSerCysPheAsnGlyThrCysValAsp 1004
QY 308 GGTCTGTGCTTTTTCAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 367
Db 1005 GlyIleAsnSerPheSerCysLeuCysProValGlyPheThrGlySerPheCysLeuHis 1024
QY 368 CAG----- 370
Db 1025 GluIleAsnGluCysSerSerHisProCysLeuAsnGluGlyThrCysValAspGlyLeu 1044

RESULT 9
US-08-532-384-19
; Sequence 19, Application US/08532384
; Patent No. 6083904
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
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QY 371 GGTCATTTTCACGCTGATGTTCTTTGGGATTC 404
| | | | | : : : | | | | | : : : | | | | : : :
Db 1045 GlyThr-TyrArgCysSerCysProLeuGlyTyr 1055

RESULT 10

US-08-899-232-1
; Sequence 1, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Oi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCES: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-899-232-1

Alignment Scores:
Pred. No.: 0.0054 Length: 2471
Score: 102.00 Matches: 42
Percent Similarity: 36.18% Conservative: 13
Best Local Similarity: 27.63% Mismatches: 48
Query Match: 11.49% Indels: 49
DB: 4 Gaps: 8

US-09-773-476-294 (1-489) x US-08-899-232-1 (1-2471)

QY 74 ATCATAGACCTTCAGGAAATCCTCTCAAGAT-----GATTGGCCAAC 118
| | | | | : : : | | | | | : : : | | | | : : :
Db 912 ILeAspAspCysLeuAlaAsnProCysGlnAsnGlySerCysMetAspGlyValAsn 931
QY 119 ACCTTCGCT-----GGGTTTACT-----CAGCTGCAGACTCTGATACTA 157
| | | | | : : : | | | | | : : : | | | | : : :
Db 932 ThrPheSerCysLeuGlyCysLeuProGlyPheThrGlyAspLysCysGlnThr----- 948
QY 158 CCACAGATGTT-----CCTGTCTCGAGGTAGTAGTAATGCTCGGAC 199
| | | | | : : : | | | | | : : : | | | | : : :
Db 949 -----AspMetAsnGluCysLeuSerGluProCysLysAsnGlyGlyThrCysSerAsp 966
QY 200 AATGTTACTTTCACAGGACAGCAGATTTGCCAAGGGCAAGGACCTTTGCATAGC 259
| | | | | : : : | | | | | : : : | | | | : : :
Db 967 TyrValAsnSerTyrThrCysLys-----CysGlnAlaGlyPheAspGlyValHisCys 984
QY 260 ACTGGAAGCCACAGAAATGTCTCTCTGAG-----AACGGATCTTTGTGCATCTGAC 307
| | | | | : : : | | | | | : : : | | | | : : :
Db 985 GluAsnAsnIleAsnGluCysThrGluSerSerCysPheAsnGlyGlyThrCysValAsp 1004
QY 308 GGTCCTGGTCTTTGCAAGTGGTTGGTGTGATGTTTCCATCGATACAGTGTATGAGG 367
| | | | | : : : | | | | | : : : | | | | : : :
Db 1005 GlyIleAsnSerPheSerCysLeuCysProValGlyPheThrGlySerPheCysLeuHis 1024
QY 368 CAG----- 370
Db 1025 GluIleAsnGluCysSerSerHisProCysLeuAsnGluGlyThrCysValAspGlyLeu 1044
QY 371 GGTCATTTTCACGCTGATGTTCTTTGGGATTC 404
| | | | | : : : | | | | | : : : | | | | : : :
Db 1045 GlyThr-TyrArgCysSerCysProLeuGlyTyr 1055

RESULT 11

US-08-185-432-19
; Sequence 19, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.

; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: ANTIBODIES, ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2703 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-185-432-19

Alignment Scores:
Pred. No.: 0.00558 Length: 2703
Score: 102.00 Matches: 25
Percent Similarity: 42.25% Conservative: 5
Best Local Similarity: 35.21% Mismatches: 29
Query Match: 11.49% Indels: 12
DB: 3 Gaps: 3

US-09-773-476-294 (1-489) x US-08-185-432-19 (1-2703)

QY 170 CCTGTCTCTGGAGTAGTAATGCTGGGACAAATGTTACTTCTTTCAAGGACAAG----- 223
| | | | | : : : | | | | | : : : | | | | : : :
Db 1229 ProCysGlnAsnGlyGlyThrCysHisAspArgValMetAsnPheSerCysSerCysPro 1248
QY 224 -----CAGATTTGCCAAGGGCAAGGACCTTTGCAATAGCCTGGAAGC 268
| | | | | : : : | | | | | : : : | | | | : : :
Db 1249 ProGlyThrMetGlyIleIleCysGluIleAsnLysAspAspCys-----Lys 1264
QY 269 CCAGAAATGTCTCTGAGACACGATCTTTGTGCATCTCCTGCTCTCTGCTTTTGCAGTGC 328
| | | | | : : : | | | | | : : : | | | | : : :
Db 1265 ProGlyAlaCysHisAsnAsnGlySerCysile---AspArgValGlyGlyPheGluCys 1283
QY 329 GTTGTGCTGATGTTTCCATGATACAGTGT 361
| | | | | : : : | | | | | : : : | | | | : : :
Db 1284 ValCysGlnProGlyPheValGlyAlaArgCys 1294
RESULT 12
US-08-899-232-4
; Sequence 4, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Oi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCES: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232

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/ CURRENT FILING DATE: 1997-07-23
/ NUMBER OF SEQ ID NOS: 4
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 2703
/ TYPE: PRI
/ ORGANISM: Drosophila sp.
/ US-08-899-232-4

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Pred. No.: 0.0058      Length: 2703
Score: 102.00          Matches: 25
Percent Similarity: 42.25%      Conservative: 5
Best Local Similarity: 35.21%    Mismatches: 29
Query Match: 11.49%             Indels: 12
DB: 4                       Gaps: 3

US-09-773-476-294 (1-489) x US-08-899-232-4 (1-2703)
QY 170 CCTGTCTGGAGGTAGTAACTCCCTGGGACAAATGTTACTTCTTCAAGGACAAG----- 223
Db 1229 ProCysGlnAsnGlyGlyThrCysHisAspArgValMetAsnPheSerCysSerCysPro 1248
QY 224 -----CAGATTGGCAAGGGCAAGGACCTTGGCAATAGCACTGGAAGC 268
Db 1249 ProGlyThrMetGlyIleLeuGlyGluLeuAsnLysAspCys-----Lys 1264
QY 269 CCAGAAATGTGCTCTGAGAACGGATCTTGTGCATCTGACGGTCTGTTTTCGAGTGC 328
Db 1265 ProGlyAlaCysHisAsnGlySerCysIle---AspArgValGlyGlyPheGluCys 1283
QY 329 GTTGTGCTGATGTTTCCATGATACAGTGT 361
Db 1284 ValCysGlnProGlyPheValGlyAlaArgCys 1294

RESULT 13
US-08-185-432-17
/ Sequence 17, Application US/08185432
/ Patent No. 5750652
/ GENERAL INFORMATION:
/ APPLICANT: Artavanis-Tsakonas, Spyridon
/ APPLICANT: Busseau, Isabelle
/ APPLICANT: Xu, Tian
/ APPLICANT: Matsuno, Kenji
/ TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
/ TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: PENNIE & EDMONDS
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/185,432
/ FILING DATE: 21-JAN-1994
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Misrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 7326-006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-8864/9741
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 17:

/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2556 amino acids
/ TYPE: amino acid
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-185-432-17

Alignment Scores:
Pred. No.: 0.00715      Length: 2556
Score: 101.00          Matches: 41
Percent Similarity: 35.19%    Conservative: 16
Best Local Similarity: 25.31%  Mismatches: 54
Query Match: 11.37%          Indels: 51
DB: 1                       Gaps: 6

US-09-773-476-294 (1-489) x US-08-185-432-17 (1-2556)
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Db 441 LeuGlnGlyThrGlyProArgCysGluIleAspValAsnGluCysValSerAsnPro 460
QY 98 CTCAAGGATGATTGGCCAAACACCTTCCTCCGGTGTCTACTCAGCTGCAGACTCTGATACTA 157
Db 461 CysGlnAsnAsp---AlaThrCysLeuAspGluIleGlyGluPheGlnCysMetCysMet 479
QY 158 CCA-----CAAGATGTTCCCTGT 175
Db 480 ProGlyThrGluGlyValHisCysGluValAsnThrAspGluCysAlaSerSerProCys 499
QY 176 CTTGGAGGTAGTAACTGCTGGGACAACTGTTACTTCTTCAAGGACAAG----- 223
Db 500 LeuHisAsnGlyArgCysLeuAspLysIleAsnGluPheGlnCysGluCysProThrGly 519
QY 224 -----CAGATTTCGCAAGGGCAAGGACCTTTGCAATAGCACTTGAAGCCAGAA 274
Db 520 PheThrGlyHisLeuCysGlnTyrAspValAspGluCysAlaSerThr----- 535
QY 275 ATGTGCTCTGAGAACGGATCTTGTGCATCTGACGGTCTGCTCTTTTGCAGTGCCTTTGT 334
Db 536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys 554
QY 335 GCTGATGTTTCCATGATACAAAGTGT----- 361
Db 555 ThrGluGlyThrGlyThrHisCysGluValAspIleAspGluCysAspProAspPro 574
QY 362 -----ATGAGCAGGGCTCATTTTCACTGCTTATGTTCTTTGGG 400
Db 575 CysHisTyrGlySerCysLysAsp-GlyValAlaThrPheThrCysLeuCysArgProG1 594
QY 401 ATTC 404
Db 594 YTYR 595

RESULT 14
US-08-083-590A-20
/ Sequence 20, Application US/08083590A
/ Patent No. 5786158
/ GENERAL INFORMATION:
/ APPLICANT: Artavanis-Tsakonas, S. et al.
/ TITLE OF INVENTION: Therapeutic And Diagnostic Methods
/ TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
/ TITLE OF INVENTION: Nucleic Acids
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,590A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2556 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-083-590A-20

Alignment Scores:
Pred. No.: 0.00715 Length: 2556
Score: 101.00 Matches: 41
Percent Similarity: 35.19% Conservative: 16
Best Local Similarity: 25.31% Mismatches: 54
Query Match: 11.37% Indels: 51
DB: Gaps: 8

US-09-773-476-294 (1-489) x US-08-083-590A-20 (1-2556)

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Db 441 LeuGlnGlyrThrGlyProArgCysGluIleAspValAsnGluCysValSerAsnPro 460
QY 98 CTCAGGATGATTGGCCACACCTTCGCGGGTTTACTCAGTCGACGACTGTGACTA 157
Db 461 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysMetCysMet 479
QY 158 CCA-----CAAGATGTTCCCTGT 175
Db 480 ProGlyTyrGluGlyValHisCysGluValAsnThrAspGluCysAlaSerProCys 499
QY 176 CTGGAGGTAGTATGCTGGACATGTACTCTTTTCAAGGACAAG-----223
Db 500 LeuHisAsnGlyArgCysLeuAspLysIleAsnGluPheGlnCysGlyProThrGly 519
QY 224 -----CAGATTGCCAAGGGCAAGGACCTTTGCAATAGCACTGGAAGCCAGAA 274
Db 520 PheThrGlyHisLeuCysGlnTyrAspValAspGluCysAlaSerThr-----535
QY 275 ATGTCCTCAGAACGGAATCTTGCAATCTGACGGTCCTGCTTTTTCAGTCGCTTGT 334
Db 536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys 554
QY 335 GCTCATGTTTCCATGATACAGTGT-----361
Db 555 ThrGluGlyTyrThrGlyThrHisCysGluValAspIleAspGluCysAspProAspPro 574
QY 362 -----ATGAGCGAGGCTCATTTTCACTGCTTATGTTCTTTGGG 400
Db 575 CysHisTyrGlySerCysLysAsp-GlyValAlaThrPheThrCysLeuCysArgProGly 594
QY 401 ATTC 404
Db 594 YTYR 595
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RESULT 15

US-08-532-384-20

; Sequence 20, Application US/08532384

; Patent No. 6083904

GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/532,384
; APPLICATION NUMBER: US/08/532,384
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/083,590
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2556 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-532-384-20

Alignment Scores:
Pred. No.: 0.00715 Length: 2556
Score: 101.00 Matches: 41
Percent Similarity: 35.19% Conservative: 16
Best Local Similarity: 25.31% Mismatches: 54
Query Match: 11.37% Indels: 51
DB: Gaps: 8

US-09-773-476-294 (1-489) x US-08-532-384-20 (1-2556)

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Db 441 LeuGlnGlyrThrGlyProArgCysGluIleAspValAsnGluCysValSerAsnPro 460
QY 98 CTCAGGATGATTGGCCACACCTTCGCGGGTTTACTCAGTCGACGACTGTGACTA 157
Db 461 CysGlnAsnAsp---AlaThrCysLeuAspGlnIleGlyGluPheGlnCysMetCysMet 479
QY 158 CCA-----CAAGATGTTCCCTGT 175
Db 480 ProGlyTyrGluGlyValHisCysGluValAsnThrAspGluCysAlaSerProCys 499
QY 176 CTGGAGGTAGTATGCTGGACATGTACTCTTTTCAAGGACAAG-----223
Db 500 LeuHisAsnGlyArgCysLeuAspLysIleAsnGluPheGlnCysGlyProThrGly 519
QY 224 -----CAGATTGCCAAGGGCAAGGACCTTTGCAATAGCACTGGAAGCCAGAA 274
Db 520 PheThrGlyHisLeuCysGlnTyrAspValAspGluCysAlaSerThr-----535
QY 275 ATGTCCTCAGAACGGAATCTTGCAATCTGACGGTCCTGCTTTTTCAGTCGCTTGT 334
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Db      536 ProCys---LysAsnGlyAlaLysCysLeuAspGlyProAsnThrTyrThrCysValCys 554
QY      335 GCTGATGGTTTCATGGATACAGTGT----- 361
Db      555 ThrGluGlyTyrThrGlyThrHisCysGluValAspIleAspGluCysAspProAspPro 574
QY      362 -----ATGAGGAGGGCTCATTTCACCTGCTTATGTTCTTTGGG 400
Db      575 CysHisTyrGlySerCysLysasp-GlyValAlaThrPheThrCysLeuCysArgProGl 594
QY      401 ATTC 404
Db      594 yTyr 595

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Job time : 28 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 25, 2004, 09:13:58 ; Search time 44.5 Seconds
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6204.556 Million cell updates/sec

Title: US-09-773-476-294

Perfect score: 888

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delopt 6.0 , Delopt 7.0

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 2327084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications AA:

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	690	77.7	229	12	US-10-245-752-8	Sequence 8, Appli
3	690	77.7	229	12	US-10-245-859-8	Sequence 8, Appli
4	690	77.7	229	13	US-10-001-054-2	Sequence 2, Appli
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43	690	77.7	229	14	US-10-245-874-8	Sequence 8, Appli
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ALIGNMENTS

RESULT 1
US-09-726-348-2
; Sequence 2, Application US/09726348
; Patent No. US200202553A1
; GENERAL INFORMATION:
; APPLICANT: Wei, Ying-Fei
; APPLICANT: et al,
; TITLE OF INVENTION: Transforming Growth Factor Alpha HIII
; FILE REFERENCE: PF220PI
; CURRENT APPLICATION NUMBER: US/09/726,348
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 08/778,545
; PRIOR FILING DATE: 1997-01-03
; PRIOR APPLICATION NUMBER: 60/011,136
; PRIOR FILING DATE: 1996-01-04
; PRIOR APPLICATION NUMBER: 60/168,387
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 229
; TYPE: BRT
; ORGANISM: homo sapiens
US-09-726-348-2

APPLICANT: Smith,Victoria
APPLICANT: Stephan,Jean-Philippe
APPLICANT: Watanabe,Colin
APPLICANT: Wood,William
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630RLC78
CURRENT APPLICATION NUMBER: US/10/245,859
CURRENT FILING DATE: 2002-09-16
PRIORITY APPLICATION NUMBER: 10/197942
PRIORITY FILING DATE: 2002-07-18
PRIORITY APPLICATION NUMBER: 60/059114
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/063046
PRIORITY FILING DATE: 1997-10-24
PRIORITY APPLICATION NUMBER: 60/065027
PRIORITY FILING DATE: 1997-11-10
PRIORITY APPLICATION NUMBER: 60/079689
PRIORITY FILING DATE: 1998-03-27
PRIORITY APPLICATION NUMBER: 60/086478
PRIORITY FILING DATE: 1998-05-22
PRIORITY APPLICATION NUMBER: 60/087607
PRIORITY FILING DATE: 1998-06-02
PRIORITY APPLICATION NUMBER: 60/089801
PRIORITY FILING DATE: 1998-06-18
PRIORITY APPLICATION NUMBER: 60/090557
PRIORITY FILING DATE: 1998-06-24
PRIORITY APPLICATION NUMBER: 60/090689
PRIORITY FILING DATE: 1998-06-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 116
SEQ ID NO 8
LENGTH: 229
TYPE: PRT
ORGANISM: Homo Sapien
US-10-245-859-8

Alignment Scores:
Pred. No.: 3,51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 12 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-859-8 (1-229)

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QY 122 TTCCTGGGTTTACTTCAGCTGAGACTCTGTATACCAAGATGTTCCCTGTCCTGGA 181
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Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192

RESULT 4

US-10-001-054-2
Sequence 2, Application US/10001054
Publication NO. US20020192209A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Baker, Kevin
APPLICANT: Goddard,Audrey
APPLICANT: Gurney,Austin
APPLICANT: Hebert,Carolyn
APPLICANT: Henzel,William
APPLICANT: Kabakoff,Rhona
APPLICANT: Shelton,David
APPLICANT: Smith,Victoria
APPLICANT: Watanabe,Colin
APPLICANT: Wood, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
FILE REFERENCE: P3034RLPCT
CURRENT APPLICATION NUMBER: US/10/001,054
CURRENT FILING DATE: 2001-11-30
PRIORITY APPLICATION NUMBER: 60/059114
PRIORITY FILING DATE: 1997-09-17
PRIORITY APPLICATION NUMBER: 60/079689
PRIORITY FILING DATE: 1998-03-27
PRIORITY APPLICATION NUMBER: 60/079920
PRIORITY FILING DATE: 1998-03-30
PRIORITY APPLICATION NUMBER: 60/082999
PRIORITY FILING DATE: 1998-04-24
PRIORITY APPLICATION NUMBER: 60/083545
PRIORITY FILING DATE: 1998-04-29
PRIORITY APPLICATION NUMBER: 60/085149
PRIORITY FILING DATE: 1998-05-12
PRIORITY APPLICATION NUMBER: 60/087607
PRIORITY FILING DATE: 1998-06-02
PRIORITY APPLICATION NUMBER: 60/088958
PRIORITY FILING DATE: 1998-06-11
PRIORITY APPLICATION NUMBER: 60/090691
PRIORITY FILING DATE: 1998-06-25
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PRIORITY FILING DATE: 1998-09-23
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PRIORITY FILING DATE: 1999-01-12
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PRIORITY APPLICATION NUMBER: 60/116533
PRIORITY FILING DATE: 1999-01-20

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; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
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; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US01/17092
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; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US01/27099
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 2
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-2

Alignment Scores:
Pred. No.: 3,51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 13 Gaps: 0

US-09-773-476-294 (1-489) x US-10-001-054-2 (1-229)
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Qy 122 TTCCTGGGTCTTACTCAGCTGAGACTCTGATCTACACAAAGATGTTCCCTGCTCTGGA 181
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Qy 242 AGGACCTTTGCAATAGCAGCTGGAAGCCCAAGATGTTCTGAGAACGATCTTGTGCA 301
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Qy 302 TCTGACGGTCTGCTGCTTTTGCAGTCCGTTGCTGCTGATGTTCCATGGATACAGTGT 361
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrlsCys 192
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RESULT 5

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US-10-245-103-8
; Sequence 8, Application US/10245103
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C112
; CURRENT APPLICATION NUMBER: US/10/245,103
; PRIOR FILING DATE: 2002-09-17
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; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-24
; PRIOR FILING DATE: 1998-06-25
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-245-103-8

Alignment Scores:
Pred. No.: 3,51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-103-8 (1-229)
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Db 93 HisThrThrValIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
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Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnProGly 132
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Qy 242 AGGACCTTTGCAATAGCAGCTGGAAGCCCAAGATGTTCTGAGAACGATCTTGTGCA 301
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
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Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgGlyAlaLys 227

RESULT 6
US-10-245-107-8
; Sequence 8, Application US/10245107
; Publication No. US20030068779A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Baton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C171
; CURRENT APPLICATION NUMBER: US/10/245,107
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
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; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
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; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-107-8

Alignment Scores:
Pred. No.: 3 51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-107-8 (1-229)
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RESULT 7
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; Sequence 8, Application US/10245143
; Publication No. US20030068780A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C90
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; CURRENT FILING DATE: 2002-09-16
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; PRIOR APPLICATION NUMBER: 60/090557
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; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-143-8

Alignment Scores:
Pred. No.: 3 51e-65 Length: 229
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Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-143-8 (1-229)
QY 3 CTGAGGCTAGATCTCAGACTGTCCTCCT-GAGATCCTGGTCCAACTTTTACAGGCT 61
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
QY 62 TATAGTCTATTATCATAGACCTTCAGGCAAACTCCTCAAGGATGTTGGCCACACC 121
Db 93 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuGlyAspLeuAlaAsnThr 112
QY 122 TTCGGTGGTTTACTCAGCTGACACTGATCTACTACCAAGATGTTCCCTGCTCTGGA 181
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132
QY 182 GGTAGTAATCCCTGGGACATGTTACTTCTTCAAGGACAGCAGATTTGCCAAGGCCAA 241
Db 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln 152
QY 242 AGGACCTTTGCAATGACATGGAAGCCAGAAATGCTCCTGAGAACGGATCTTTGTGCA 301
```


Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
QY 302 TCTGACGGTCTGCTGCTTTTGCAGTGCCTTTGCTGCTGATGTTCCATGGATACAAAGTGT 361
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192
QY 362 ATGAGCGAGGCTCATTTTCACTGCTTATGTTCTTTGGGATTCGGGATCCACCAAGCTA 421
Db 193 MetAsgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
QY 422 GCCATCTNCATCTACTTTGGGAAACCCAGCGCCGGAAGCAAG 466
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgAsgLysAlaLys 227

RESULT 8
US-10-245-771-8
; Sequence 8, Application US/10245771
; Publication No. US20030068781A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C98
; CURRENT APPLICATION NUMBER: US/10/245,771
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-771-8

Alignment Scores:
Pred. No.: 3,51e-65
Score: 690.00
Matches: 128
Conservative: 11
Best Local Similarity: 89.68%
Query Match: 82.58%
Indels: 16
Gaps: 1
DB: 0

US-09-773-476-294 (1-489) x US-10-245-771-8 (1-229)
QY 3 CTGAGGCTAGATCTTCTGAGACTGTTCCCT- GAGGATCTGCTGCTCAAACTTTTACAGGCT 61
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
QY 62 TATACTGCTATTATCATAGACCTTTCAGGCAAACTCTCTCAAGGATGATTGGCCAAACACC 121
Db 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
QY 122 TTCCGTGGGTTTACTGAGTGCAGACTCTGATCTACTATACCACCAAGATGTTCCCTGCTCTGGA 191
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132
QY 182 GGTAGTAATGCTGGGCAAACTGTTACTTCTTCAAGCAACAAGCAGATTTCCCAAGGSCAA 241
Db 133 GlyIleAsnAlaTrpAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln 152
QY 242 AGGACCTTTTGCATAGCACTGGAAGCCCAAGAAATGTCTCTGAGAACGGATCTTGTGCA 301
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
QY 302 TCTGACGGTCTGCTGCTTTTGCAGTGGTGTGCTGATGGTTCATGATGATCAACAGTGT 361
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192
QY 362 ATGAGCGAGGCTCATTTTCACTGCTTATGTTCTTTGGGATTCGGGATCCACCAAGCTA 421
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
QY 422 GCCATCTNCATCTACTTTGGGAAACCCAGCGCCGGAAGCAAG 466
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgAsgLysAlaLys 227

RESULT 9
US-10-245-851-8
; Sequence 8, Application US/10245851
; Publication No. US20030068782A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C93
; CURRENT APPLICATION NUMBER: US/10/245,851
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557

;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090689
;; PRIOR FILING DATE: 1998-06-25
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 116
;; SEQ ID NO 8
;; LENGTH: 229
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-245-851-8

Alignment Scores:
Pred. No.: 3,51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-851-8 (1-229)

Qy 3 CTGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGGTCCAAACTTTTACAGGCT 61
Db |||||
73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
Qy 62 TATACTGCTATTATCATAGACCTTCAGGCAAACTCTCAAGGATGATTGGCCACACC 121
Db |||||
93 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
Qy 122 TTCGCTGGGTTTACTCAGCTGCAGACTCTCATACTACTACCAAGATGTTCCCTGCTCGGA 181
Db |||||
113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132
Qy 182 GGTAGTAATGCTGGGACAATGTTACTTCTTCAAGCAAGCAGATTTGCCAAGGGCAA 241
Db |||||
133 GlyIleAsnAlaThrAsnThrIleThrSerTyIleAspAsnGlnIleCysGlnGlyGln 152
Qy 242 AGGACCTTTGCATAGCAGCTGCAGCCAGCAATCTCTCAGGATGATTGGCCACACC 301
Db |||||
153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
Qy 302 TCTGACGCTCCTGGTCTTTTGCAGTGGTTGTGCTGATGGTTTCCATGGATACAGTGT 361
Db |||||
173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyLysCys 192
Qy 362 ATGAGGAGGGCTCATTTTACGCTTATGTTCTTTGGGATTTCTGGATCCACAGCTA 421
Db |||||
193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyLeuGlyAlaThrThrLeu 212
Qy 422 GCCATCTNCATTCTACTTTGGGAAACCCAGCGCCGGAAGCCCAAG 466
Db |||||
213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227

RESULT 10

US-10-245-883-8
; Sequence 8, Application US/10245883
; Publication No. US20030068783A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C70

;; CURRENT APPLICATION NUMBER: US/10/245,883
;; CURRENT FILING DATE: 2002-09-16
;; PRIOR APPLICATION NUMBER: 10/197942
;; PRIOR FILING DATE: 2002-07-18
;; PRIOR APPLICATION NUMBER: 60/059114
;; PRIOR FILING DATE: 1997-09-17
;; PRIOR APPLICATION NUMBER: 60/063046
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/065027
;; PRIOR FILING DATE: 1997-11-10
;; PRIOR APPLICATION NUMBER: 60/079689
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/086478
;; PRIOR FILING DATE: 1998-05-22
;; PRIOR APPLICATION NUMBER: 60/087607
;; PRIOR FILING DATE: 1998-06-02
;; PRIOR APPLICATION NUMBER: 60/089801
;; PRIOR FILING DATE: 1998-06-18
;; PRIOR APPLICATION NUMBER: 60/090557
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090689
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 116
;; SEQ ID NO 8
;; LENGTH: 229
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-245-883-8

Alignment Scores:
Pred. No.: 3,51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-883-8 (1-229)

Qy 3 CTGAGGCTAGATCTTCAGAACTGTTCCCT-GAGGATCCTGGTCCAAACTTTTACAGGCT 61
Db |||||
73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
Qy 62 TATACTGCTATTATCATAGACCTTCAGGCAAACTCTCTCAGGATGATTGGCCACACC 121
Db |||||
93 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
Qy 122 TTCGCTGGGTTTACTCAGCTGCAGACTCTGATACCAAGATGTTCCCTGCTCTCGGA 181
Db |||||
113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuLeuProGlnHisValAsnCysProGly 132
Qy 182 GGTAGTAATGCTGGGACAATGTTACTTCTTCAAGCAAGCAGATTTGCCAAGGGCAA 241
Db |||||
133 GlyIleAsnAlaThrAsnThrIleThrSerTyIleAspAsnGlnIleCysGlnGlyGln 152
Qy 242 AGGACCTTTGCATAGCAGCTGCAGCCAGCAATCTCTCAGGATGATTGGCCACACC 301
Db |||||
153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
Qy 302 TCTGACGCTCCTGGTCTTTTGCAGTGGTTGTGCTGATGGTTTCCATGGATACAGTGT 361
Db |||||
173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyLysCys 192
Qy 362 ATGAGGAGGGCTCATTTTACGCTTATGTTCTTTGGGATTTCTGGATCCACAGCTA 421
Db |||||
193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyLeuGlyAlaThrThrLeu 212
Qy 422 GCCATCTNCATTCTACTTTGGGAAACCCAGCGCCGGAAGCCCAAG 466
Db |||||
213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227

RESULT 11

US-10-237-535-8
; Sequence 8, Application US/10237535
; Publication No. US20030073188A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630RIC3
; CURRENT APPLICATION NUMBER: US/10/237,535
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-03-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091358
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/106932
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 60/115554
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/119342
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/123957
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123972
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: 60/127372
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/131271
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/133459
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/135725
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/135729
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138385
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/140653
; PRIOR FILING DATE: 1999-06-22
; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144732
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/144790
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145228
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146843
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/148188
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: 60/148513
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/149327
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149395
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; PRIOR APPLICATION NUMBER: 60/150114
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/151700
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/151734
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/177118
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: 60/179851
; PRIOR FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 60/180921
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/187202
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/198587
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: 60/199614
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 60/206330
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/206368
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/209832
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/218371
; PRIOR FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 60/222695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/229896
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/230621
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/235147
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/261878
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 60/261910
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/261939
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/262150
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/264395

1	PRIOR FILING DATE: 2001-01-25	
2	PRIOR APPLICATION NUMBER: 607266421	
3	PRIOR FILING DATE: 2001-02-02	
4	PRIOR APPLICATION NUMBER: 607266231	
5	PRIOR FILING DATE: 2001-02-09	
6	PRIOR APPLICATION NUMBER: 607274399	
7	PRIOR FILING DATE: 2001-03-09	
8	PRIOR APPLICATION NUMBER: 607280982	
9	PRIOR FILING DATE: 2001-04-03	
10	PRIOR APPLICATION NUMBER: 607282129	
11	PRIOR FILING DATE: 2001-04-04	
12	PRIOR APPLICATION NUMBER: 607282199	
13	PRIOR FILING DATE: 2001-04-04	
14	PRIOR APPLICATION NUMBER: 607290588	
15	PRIOR FILING DATE: 2001-05-09	
16	PRIOR APPLICATION NUMBER: 607180997	
17	PRIOR FILING DATE: 1998-11-19	
18	PRIOR APPLICATION NUMBER: 097267213	
19	PRIOR FILING DATE: 1999-03-12	
20	PRIOR APPLICATION NUMBER: 097380137	
21	PRIOR FILING DATE: 1999-08-25	
22	PRIOR APPLICATION NUMBER: 097380138	
23	PRIOR FILING DATE: 1999-08-25	
24	PRIOR APPLICATION NUMBER: 097403297	
25	PRIOR FILING DATE: 1999-10-18	
26	PRIOR APPLICATION NUMBER: 097423741	
27	PRIOR FILING DATE: 1999-11-10	
28	PRIOR APPLICATION NUMBER: 097709238	
29	PRIOR FILING DATE: 2000-11-08	
30	PRIOR APPLICATION NUMBER: 097802706	
31	PRIOR FILING DATE: 2001-03-09	
32	PRIOR APPLICATION NUMBER: 097872035	
33	PRIOR FILING DATE: 2001-06-01	
34	PRIOR APPLICATION NUMBER: 097918585	
35	PRIOR FILING DATE: 2001-07-30	
36	PRIOR APPLICATION NUMBER: 097924419	
37	PRIOR FILING DATE: 2001-08-06	
38	PRIOR APPLICATION NUMBER: 097927796	
39	PRIOR FILING DATE: 2001-08-09	
40	PRIOR APPLICATION NUMBER: 097929404	
41	PRIOR FILING DATE: 2001-08-13	
42	PRIOR APPLICATION NUMBER: 097931836	
43	PRIOR FILING DATE: 2001-08-16	
44	PRIOR APPLICATION NUMBER: 097941992	
45	PRIOR FILING DATE: 2001-08-28	
46	PRIOR APPLICATION NUMBER: 097946374	
47	PRIOR FILING DATE: 2001-09-04	
48	PRIOR APPLICATION NUMBER: 107001054	
49	PRIOR FILING DATE: 2001-11-30	
50	PRIOR APPLICATION NUMBER: 107052586	
51	PRIOR FILING DATE: 2002-01-15	
52	PRIOR APPLICATION NUMBER: 107081056	
53	PRIOR FILING DATE: 2002-02-20	
54	PRIOR APPLICATION NUMBER: 107119480	
55	PRIOR FILING DATE: 2002-04-09	

US-09-773-476-294 (1-489) x US-10-237-535-8 (1-229)

QY	3	CTGAGGCTAGATCTTCAGAACTGTTCCCT	-	GAGGATCCTGGTCCAAACTTTTTTACAGGCT	61
Db	73	LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsn	-	ProHisGlnAla	92
QY	62	TATACTGCTATTATCATAGACTTCAGGCAAACTCCTCTCAAGGATGATTTGGCCAAACACC	-		121
Db	93	HisThrValIleIleAspLeuGlnAlaAsnProLeuGlyAspLeuAlaAsnThr	-		112

;; PRIOR APPLICATION NUMBER: 60/106932
;; PRIOR FILING DATE: 1998-11-03
;; PRIOR APPLICATION NUMBER: 60/115554
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119342
;; PRIOR FILING DATE: 1999-02-09
;; PRIOR APPLICATION NUMBER: 60/123957
;; PRIOR FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: 60/123972
;; PRIOR FILING DATE: 1999-03-11
;; PRIOR APPLICATION NUMBER: 60/127372
;; PRIOR FILING DATE: 1999-04-01
;; PRIOR APPLICATION NUMBER: 60/131271
;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/133459
;; PRIOR FILING DATE: 1999-05-11
;; PRIOR APPLICATION NUMBER: 60/135725
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: 60/135729
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: 60/135750
;; PRIOR FILING DATE: 1999-05-25
;; PRIOR APPLICATION NUMBER: 60/138385
;; PRIOR FILING DATE: 1999-06-09
;; PRIOR APPLICATION NUMBER: 60/140653
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/144732
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/144790
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145228
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: 60/146222
;; PRIOR FILING DATE: 1998-07-28
;; PRIOR APPLICATION NUMBER: 60/146843
;; PRIOR FILING DATE: 1999-08-03
;; PRIOR APPLICATION NUMBER: 60/148188
;; PRIOR FILING DATE: 1999-08-10
;; PRIOR APPLICATION NUMBER: 60/148513
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;; PRIOR APPLICATION NUMBER: 60/149327
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/149395
;; PRIOR FILING DATE: 1999-08-17
;; PRIOR APPLICATION NUMBER: 60/150114
;; PRIOR FILING DATE: 1999-08-20
;; PRIOR APPLICATION NUMBER: 60/151700
;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/151734
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;; PRIOR APPLICATION NUMBER: 60/162506
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;; PRIOR APPLICATION NUMBER: 60/170262
;; PRIOR FILING DATE: 1999-12-09
;; PRIOR APPLICATION NUMBER: 60/177118
;; PRIOR FILING DATE: 2000-01-20
;; PRIOR APPLICATION NUMBER: 60/179851
;; PRIOR FILING DATE: 2000-02-02
;; PRIOR APPLICATION NUMBER: 60/180921
;; PRIOR FILING DATE: 2000-02-08
;; PRIOR APPLICATION NUMBER: 60/187202
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;; PRIOR APPLICATION NUMBER: 60/198587
;; PRIOR FILING DATE: 2000-04-18
;; PRIOR APPLICATION NUMBER: 60/199614
;; PRIOR FILING DATE: 2000-04-25
;; PRIOR APPLICATION NUMBER: 60/206330
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/206368
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/209832
;; PRIOR FILING DATE: 2000-06-05
;; PRIOR APPLICATION NUMBER: 60/218371
;; PRIOR FILING DATE: 2000-07-13
;; PRIOR APPLICATION NUMBER: 60/222695
;; PRIOR FILING DATE: 2000-08-02
;; PRIOR APPLICATION NUMBER: 60/229896
;; PRIOR FILING DATE: 2000-09-01
;; PRIOR APPLICATION NUMBER: 60/230621
;; PRIOR FILING DATE: 2000-09-05
;; PRIOR APPLICATION NUMBER: 60/232887
;; PRIOR FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: 60/235147
;; PRIOR FILING DATE: 2000-09-22
;; PRIOR APPLICATION NUMBER: 60/261878
;; PRIOR FILING DATE: 2001-01-12
;; PRIOR APPLICATION NUMBER: 60/261910
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: 60/261939
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: 60/262150
;; PRIOR FILING DATE: 2001-01-16
;; PRIOR APPLICATION NUMBER: 60/264395
;; PRIOR FILING DATE: 2001-01-25
;; PRIOR APPLICATION NUMBER: 60/266421
;; PRIOR FILING DATE: 2001-02-02
;; PRIOR APPLICATION NUMBER: 60/267623
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/274399
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 60/280982
;; PRIOR FILING DATE: 2001-04-03
;; PRIOR APPLICATION NUMBER: 60/282129
;; PRIOR FILING DATE: 2001-04-04
;; PRIOR APPLICATION NUMBER: 60/282199
;; PRIOR FILING DATE: 2001-04-04
;; PRIOR APPLICATION NUMBER: 60/290589
;; PRIOR FILING DATE: 2001-05-09
;; PRIOR APPLICATION NUMBER: 09/180997
;; PRIOR FILING DATE: 1998-11-19
;; PRIOR APPLICATION NUMBER: 09/267213
;; PRIOR FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: 09/380137
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/403297
;; PRIOR FILING DATE: 1999-10-18
;; PRIOR APPLICATION NUMBER: 09/423741
;; PRIOR FILING DATE: 1999-11-10
;; PRIOR APPLICATION NUMBER: 09/709238
;; PRIOR FILING DATE: 2000-11-08
;; PRIOR APPLICATION NUMBER: 09/802706
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: 09/872035
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 09/924419
;; PRIOR FILING DATE: 2001-08-06
;; PRIOR APPLICATION NUMBER: 09/927796
;; PRIOR FILING DATE: 2001-08-09
;; PRIOR APPLICATION NUMBER: 09/929404
;; PRIOR FILING DATE: 2001-08-13
;; PRIOR APPLICATION NUMBER: 09/931836
;; PRIOR FILING DATE: 2001-08-16
;; PRIOR APPLICATION NUMBER: 09/941992
;; PRIOR FILING DATE: 2001-08-28
;; PRIOR APPLICATION NUMBER: 09/946374
;; PRIOR FILING DATE: 2001-09-04

; PRIOR APPLICATION NUMBER: 10/001054
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/081056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: 10/119480
; PRIOR FILING DATE: 2002-04-09

Alignment Scores:
Pred. No.: 3 51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservativity: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-238-183-8 (1-229)

QY 3 CTGAGGCTAGATCTTCAGACTGTTCCCT-CAGGATCTCGTCCAACTTTTACAGGCT 61
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92

QY 62 TATACCTGCTATTATCATAGACCTTCAGGCAAACTCTCAAGGATGATTGGCCAAACACC 121
Db 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112

QY 122 TTCGGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGCTCTGGA 181
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnCysProGly 132

QY 182 GGTAGTAAATGCTGGGACAATGTTACTTCTTCAAGGACAAGCAGATTTGCCAAGGCCAA 241
Db 133 GlyIleAsnAlaTrpAsnThrIleThrSerTy-IleAspAsnGlnIleCysGlnGlyGln 152

QY 242 AGGACCTTTGCAATAGCACTGGAAGCCCAAGAAATGTCTCAGAACCGGATCTTGTCGA 301
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172

QY 302 TCTGACGCTCTGCTCTTTTGGCAGTGGTGTGCTGATGCTGATGCTTCCATGGATACAGTGT 361
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyIysCys 192

QY 362 ATGAGCAGGCTCATTTTCATCTGCTTATGTTCTTTGGGATTTCCGATCCACCGCTA 421
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212

QY 422 GCCATCTNCATCTACTTTGGGAAACCCAGCCGCGGAAAGCCAAAG 466
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227

RESULT 13
US-10-238-283-8
; Sequence 8, Application US/10238283
; Publication No. US20030073190A1
GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3630R1C15
; CURRENT APPLICATION NUMBER: US/10/238,283
; CURRENT FILING DATE: 2002-09-09

; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-238-283-8

Alignment Scores:
Pred. No.: 3 51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservativity: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-238-283-8 (1-229)

QY 3 CTGAGGCTAGATCTTCAGACTGTTCCCT-CAGGATCTCGTCCAACTTTTACAGGCT 61
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92

QY 62 TATACCTGCTATTATCATAGACCTTCAGGCAAACTCTCAAGGATGATTGGCCAAACACC 121
Db 93 HisThrThrValIleIleAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112

QY 122 TTCGGTGGGTTTACTCAGCTGCAGACTCTGATACCTACCAAGATGTTCCCTGCTCTGGA 181
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuLeuProGlnHisValAsnCysProGly 132

QY 182 GGTAGTAAATGCTGGGACAATGTTACTTCTTCAAGGACAAGCAGATTTGCCAAGGCCAA 241
Db 133 GlyIleAsnAlaTrpAsnThrIleThrSerTy-IleAspAsnGlnIleCysGlnGlyGln 152

QY 242 AGGACCTTTGCAATAGCACTGGAAGCCCAAGAAATGTCTCAGAACCGGATCTTGTCGA 301
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172

QY 302 TCTGACGCTCTGCTCTTTTGGCAGTGGTGTGCTGATGCTGATGCTTCCATGGATACAGTGT 361
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyIysCys 192

QY 362 ATGAGCAGGCTCATTTTCATCTGCTTATGTTCTTTGGGATTTCCGATCCACCGCTA 421
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212

QY 422 GCCATCTNCATCTACTTTGGGAAACCCAGCCGCGGAAAGCCAAAG 466
Db 213 SerValSerIleLeuLeuTrpAlaThrGlnArgArgLysAlaLys 227

RESULT 14
US-10-238-370-8
; Sequence 8, Application US/10238370

Publication No. US20030073191A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C10
; CURRENT APPLICATION NUMBER: US/10/238,370
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-238-370-8

Alignment Scores:
Pred. No.: 3 51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-238-370-8 (1-229)
QY 3 CTGAGCTAGACTTCAGAACTGTCCT- GAGGATCCGTGTCACAACTTTTACAGCT 61
Db 73 LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla 92
QY 62 TATACGCTATTATCATACACTTCAGCAAACTCTCTCAAGGATGATTGGCCACACC 121
Db 93 HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyAspLeuAlaAsnThr 112
QY 122 TTCCTGGGTTTACTCAGCTGACACTTCGAGCACTCTGATCTACCAAGATGTTCCCTGCTCTGGA 181
Db 113 PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly 132
QY 182 GGTAGTAATGCTGGACAACTTACTTCTTTCAGGACAAACAGATTTGCCAAGGGA 241
Db 133 GlyIleAsnAlaIleAsnThrIleThrSerTyrIleAspAsnGlnIleCysGlnGlyGln 152

QY 242 AGGACCTTTGCAATAGCACTGGAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCA 301
Db 153 LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal 172
QY 302 TCTGACGGTCTCTGCTCTTTTTCAGTGGCTTTGTCTGCTGATGTTTCCATGGATACAAAGTGT 361
Db 173 ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys 192
QY 362 ATGAGGAGGGCTCATTTTCTACTCTTATGTTCTTCTGGATTTCTGGATTCACACGCTA 421
Db 193 MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu 212
QY 422 GCCATCTNCATTTCTACTTTGGGAACCCAGCGCGGAAAGCAAG 466
Db 213 SerValSerIleLeuLeuThrAlaThrGluArgArgLysAlaLys 227

RESULT 15
US-10-245-055-8
; Sequence 8, Application US/10245055
; Publication No. US20030073192A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Eaton, Dan
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Phillippe
; APPLICANT: Watanabe, Colin
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; APPLICANT: Fong, Sherman
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3630R1C88
; CURRENT APPLICATION NUMBER: US/10/245,055
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: 10/197942
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/059114
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/063046
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/065027
; PRIOR FILING DATE: 1997-11-10
; PRIOR APPLICATION NUMBER: 60/079689
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/086478
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090689
; PRIOR FILING DATE: 1998-06-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 116
; SEQ ID NO 8
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-245-055-8

Alignment Scores:
Pred. No.: 3 51e-65 Length: 229
Score: 690.00 Matches: 128
Percent Similarity: 89.68% Conservative: 11
Best Local Similarity: 82.58% Mismatches: 16
Query Match: 77.70% Indels: 1
DB: 14 Gaps: 0

US-09-773-476-294 (1-489) x US-10-245-055-8 (1-229)

Qy	3	CTGAGGCTAGATCTTCAGAACTGTTCCT-GAGGATCCTGGTCCAAACTTTTACAGGCT	61
Db	73	LeuGlyLeuAspLeuGlnAsnCysSerLeuGluAspProGlyProAsnPheHisGlnAla	92
Qy	62	TATACTCTATTATCATAGACCTTCAGGCAAAATCCTCTCAAGGATGATTGGCCAAACACC	121
Db	93	HisThrThrValIleLeuAspLeuGlnAlaAsnProLeuLysGlyLeuAlaAsnThr	112
Qy	122	TTCCGTGGGTCTACTGCTGACACTCTGATCTACTACCAAGATGTTCCCTGCTCTGGA	181
Db	113	PheArgGlyPheThrGlnLeuGlnThrLeuIleLeuProGlnHisValAsnCysProGly	132
Qy	182	GGTAGTAATGCTGGGACAATGTTACTTCTTCAAGGACAAAGCAGATTTGCCAAGGGCAA	241
Db	133	GlyIleAsnAlaTrpAsnThrIleThrSerTy-IleAspAsnGlnIleCysGlnGlyGln	152
Qy	242	AGGACCTTTGCATAGCACTGAGAGCCAGAAATGTCTCTGAGAACGGATCTTGTGCA	301
Db	153	LysAsnLeuCysAsnAsnThrGlyAspProGluMetCysProGluAsnGlySerCysVal	172
Qy	302	TCTCACGGTCTGTCTTTTGCAGTGGCTTTGTGCTGATGGTTTCCATGGATACAAGTGT	361
Db	173	ProAspGlyProGlyLeuLeuGlnCysValCysAlaAspGlyPheHisGlyTyrLysCys	192
Qy	362	ATGAGCAGGGCTCATTTTCACTGCTTATGTTCTTTGGGATCTGGGATCCACACGCTA	421
Db	193	MetArgGlnGlySerPheSerLeuLeuMetPhePheGlyIleLeuGlyAlaThrThrLeu	212
Qy	422	GCCATCTNCATTTCTACTTTGGGGAACCCAGCGCGGAAGCCCAAG	466
Db	213	SerValSerIleLeuLeuTrpAlaThrGlnArgLysAlaLys	227

Search completed: June 25, 2004, 09:19:32
Job time : 47.5 secs